

SEQUENCE LISTING



<110> Goodman, Corey S.
Kidd, Thomas
Mitchell, Kevin J.
Tear, Guy
The Regents of the University of California

<120> ROBO: A Novel Family of Polypeptides and Nucleic Acids

<130> 18941H-002911US

<140> US 10/826,812

<141> 2004-04-16

<150> US 60/062,921

<151> 1997-10-20

<150> US 08/971,172

<151> 1997-11-14

<160> 92

<170> PatentIn Ver. 2.1

<210> 1

<211> 4188

<212> DNA

<213> *Drosophila melanogaster*

<220>

<223> *Drosophila roundabout (robo) 1 cDNA*

<400> 1

```

atgcatccca tgcattcccga aaaccacgcc atcgcccggga gcacgagcac cactaataaac 60
ccatctcgca gtcggagcag caggatgtgg ctccgtgccg cctggctgct cctcgctcctg 120
gtggccagca atggcctgcc agcagtcaga ggccagtacc aatcgccacg tatcatcgag 180
catcccacgg atctggctcgt taagaagaat gaaccgcgca cgctcaactg caaagtggag 240
ggcaagccgg aacccaccat tgagtgggtt aaggatggcg aaccgcgcag caccaacgaa 300
aagaaatcgc accgcgtcca gttcaaggac ggcgcctctt tcttttacag gacaatgcaa 360
ggcaagaagg agcaggacgg cggagagtag tgggtgcgtg ccaagaaccg agtgggcccag 420
gccgttagtc gccatgcctc cctccagata gctgttttgc gcgacgattt tcgctggag 480
cccaagaca cgcgagtggc caaaggcgag acggctctgc tggagtgtgg gccgccccaa 540
ggcattccag agccaacgct gatttgata aaggacggcg ttcccttggg cgacctgaaa 600
gccatgtcgt ttggcgccag ctccgcgctt cgaattgtgg acggtggcaa cctgctgata 660
agcaatgtgg agcccattga tgagggcaac tacaagtga ttgcccagaa tctggtaggc 720
accgcgcgag gcagctatgc caagctgatt gtccaggtca aaccatactt tatgaaggag 780
cccaaggatc aggtgatgct ctacggccag acagccactt tccactgctc agtgggcccgt 840
gatccgcccgc gaaagtgtt gtggaaaaag gaggagggca atattccggt gtccagagcg 900
cgaatccttc acgacgagaa aagtttagag atatccaaca taacgcccac cgatgagggc 960
acctatgtct gcgaggcaca caacaatgtc ggtcagatca agcgtagggc ttctcttata 1020
gtccacgctc cgccgaactt tacgaaaaga cccagtaaca agaaagtggg actaaatggg 1080
gttggtccaac taccttgcac ggccctccga aaccctccgc cgtctgtatt ctggaccaag 1140
gaaggagtat ccaactctat gttcccaaat agttcgacg gaaggcagta tgtggctgcc 1200
gatggaactc tgcagattac ggatgtgcgg caggagacg aaggctacta tgtgtgttcc 1260
gctttcagtg tagtcgattc ctctacagta cgggttttcc tgcaagtacg ctcggtagac 1320
gagcgtccac ctccgattat tcaaatcgga cctgccaatc aaacactgcc caagggatca 1380
gttgctactt taccctgtcg ggccactgga aatcccagtc cccgtatcaa gtgggtccac 1440
gatggacatg ccgtacaagc gggcaatcga tacagcatca tccaaggaag ctactgaga 1500
gtcgatgacc ttcaactaag tgactctggt acctacacct gcactgcac tggcgaacga 1560
ggagaaactt cctgggctgc cacactaacg gtggaaaaac ccggttctac atctcttcac 1620

```

cgggcagctg	atcctagcac	ttatcctgct	cctccaggaa	cacctaaagt	cctgaatgtc	1680
agtcgcacca	gcattagtct	tcgttgggct	aaaagccaag	agaaacccgg	agctgtgggc	1740
ccaatcattg	gatacactgt	agagtacttc	agtccggatc	tgcaaactgg	ttggattgtg	1800
gctgcccatac	gagtcggcga	cactcaagtc	actatctcgg	gtctcactcc	tggcacttcg	1860
tatgtgttcc	tagttagagc	tgagaatact	cagggtatct	ctgtgccttc	cggcttatca	1920
aatgttatta	aaaccattga	ggcagatttc	gatgcagctt	ctgccaatga	tttgtcagca	1980
gctcgaactt	tgctgacagg	aaagtcgggtg	gagctaatag	atgcctcggc	tatcaatgct	2040
agtgccgtta	gacttgagtg	gatgctccac	gtgagcgctg	atgagaaata	cgtagagggc	2100
ctgcgcatatc	actataagga	tgccagtgtg	ccatccgcac	agtatcactc	gatcactgtt	2160
atggatgcct	ctgcagaatc	gtttgtgggtg	ggaaacctta	agaagtacac	caagtatgag	2220
ttcttcctaa	cacctttttt	tgagacaatt	gaaggacagc	ccagtaactc	caagacagcc	2280
ctcacctatg	aagatgttcc	ctccgcacca	ccggataaca	ttcagattgg	catgtacaac	2340
caaacgcacg	gttgggtgcg	ttggactccg	ccacctccc	agcaccacaa	tggcaatttg	2400
tatggctaca	agattgaggt	cagcgccggt	aacaccatga	aggtgctggc	caatatgact	2460
cttaatgcta	ccaccacatc	tgtgctccta	aataacctaa	ccaccggagc	tgtgtacagc	2520
gtgaggttga	actcctttac	caaggcagga	gatggacctt	actccaaacc	gatatcacta	2580
ttcatggacc	ccaccatca	tgtgcatccg	ccacgggcac	atccaagcgg	cacccatgat	2640
gggcgacatg	agggacagga	tctcacgtat	cataacaatg	gcaacatacc	acctggcgac	2700
attaatccca	ccactcataa	aaagaccact	gactacctat	ctggaccgtg	gctaattggtg	2760
ctggtctgca	tcgttcttct	agtcctgggt	atttcggcgg	ctatttcgat	ggtctacttc	2820
aagcgcaagc	atcaaattgac	caaggaattg	ggtcacttaa	gtgtgggtcag	tgacaacgaa	2880
ataaccgcgt	taaatatcaa	tagcaaagag	agcctttgga	tagaccatca	tcgtggatgg	2940
cgaactgccc	atactgacaa	agactcagga	ttaagcgaat	cgaagctact	atcccacgtt	3000
aacagcagtc	aatccaacta	caataactcc	gatggaggaa	ccgatttatgc	agaagttgac	3060
acccgtaacc	ttaccacctt	ctacaattgt	cgcaagagcc	ccgataatcc	cacgccgtac	3120
gccaccacta	tgatcattgg	tacctcttcc	agtgagacct	gcaccaagac	aacatctata	3180
agtgccgata	aggactcggg	aactcattcg	ccctattctg	acgcatttgc	cggtcagggtg	3240
ccagcgggtt	ctgttgtcaa	atccaactat	cttcagtatc	cggttgaacc	gatcaactgg	3300
tcagagtttc	tacccccgcc	gccagaacac	ccacctccgt	cttctaccta	tggatacgca	3360
caaggatctc	ctgaatcttc	gcggaagagc	tccaaaagcg	caggttccgg	catttctaca	3420
aatcaaagca	ttctgaacgc	atccatacac	agcagctcct	cgggcgggct	ttcagcttgg	3480
ggagtatcgc	cccaatatgc	tgtcgccgtg	ccaccggaaa	acgtttatag	caatccgctg	3540
tcggcagtg	ctggcggcac	ccagaaccgc	tatcagataa	cgcccacaaa	ccaacatccg	3600
ccacagttac	cggcctactt	tgccaccacg	ggtccaggag	gagctgtacc	acccaaccac	3660
ctgccatttg	ccacacagcg	tcattgcagc	agcgagtacc	aggctggact	gaatgcagcg	3720
cgatgtgccc	aaagccgcgc	ctgcaacagc	tgcgatgcct	tggccacacc	ctcgcccatg	3780
caacccccac	cgccagttcc	cgtacccgag	ggctggtacc	aaccggtgca	tcccaatagc	3840
cacccgatgc	acccgacctc	ctccaaccac	cagatctacc	agtgtcctc	cgagtgtctg	3900
gatcactcga	ggagctcgca	gagtcacaag	cggcagctgc	agctcgagga	gcacggcagc	3960
agtgccaaac	aacgcggagg	acaccaccgt	cgacgagccc	cgggtggtgca	gccgtgcatg	4020
gagagcgaga	acgagaacat	gctggcggag	tacgagcagc	gccagtacac	cagcgattgc	4080
tgcaatagct	cccgcgaggg	cgacacctgc	tctgacagcg	agggatcctg	tctttacgcc	4140
gaggcgggcg	agccggcgcc	tcgtcaaatg	actgctaaga	acacctaa		4188

<210> 2

<211> 1395

<212> PRT

<213> *Drosophila melanogaster*

<220>

<223> *Drosophila roundabout (robo) 1 (D1) protein*

<400> 2

Met	His	Pro	Met	His	Pro	Glu	Asn	His	Ala	Ile	Ala	Arg	Ser	Thr	Ser
1				5					10					15	

Thr	Thr	Asn	Asn	Pro	Ser	Arg	Ser	Arg	Ser	Ser	Arg	Met	Trp	Leu	Leu
		20					25					30			

Pro Ala Trp Leu Leu Leu Val Leu Val Ala Ser Asn Gly Leu Pro Ala
 35 40 45
 Val Arg Gly Gln Tyr Gln Ser Pro Arg Ile Ile Glu His Pro Thr Asp
 50 55 60
 Leu Val Val Lys Lys Asn Glu Pro Ala Thr Leu Asn Cys Lys Val Glu
 65 70 75 80
 Gly Lys Pro Glu Pro Thr Ile Glu Trp Phe Lys Asp Gly Glu Pro Val
 85 90 95
 Ser Thr Asn Glu Lys Lys Ser His Arg Val Gln Phe Lys Asp Gly Ala
 100 105 110
 Leu Phe Phe Tyr Arg Ile Met Gln Gly Lys Lys Glu Gln Asp Gly Gly
 115 120 125
 Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln Ala Val Ser Arg
 130 135 140
 His Ala Ser Leu Gln Ile Ala Val Leu Arg Asp Asp Phe Arg Val Glu
 145 150 155 160
 Pro Lys Asp Thr Arg Val Ala Lys Gly Glu Thr Ala Leu Leu Glu Cys
 165 170 175
 Gly Pro Pro Lys Gly Ile Pro Glu Pro Thr Leu Ile Trp Ile Lys Asp
 180 185 190
 Gly Val Pro Leu Asp Asp Leu Lys Ala Met Ser Phe Gly Ala Ser Ser
 195 200 205
 Arg Val Arg Ile Val Asp Gly Gly Asn Leu Leu Ile Ser Asn Val Glu
 210 215 220
 Pro Ile Asp Glu Gly Asn Tyr Lys Cys Ile Ala Gln Asn Leu Val Gly
 225 230 235 240
 Thr Arg Glu Ser Ser Tyr Ala Lys Leu Ile Val Gln Val Lys Pro Tyr
 245 250 255
 Phe Met Lys Glu Pro Lys Asp Gln Val Met Leu Tyr Gly Gln Thr Ala
 260 265 270
 Thr Phe His Cys Ser Val Gly Gly Asp Pro Pro Pro Lys Val Leu Trp
 275 280 285
 Lys Lys Glu Glu Gly Asn Ile Pro Val Ser Arg Ala Arg Ile Leu His
 290 295 300
 Asp Glu Lys Ser Leu Glu Ile Ser Asn Ile Thr Pro Thr Asp Glu Gly
 305 310 315 320
 Thr Tyr Val Cys Glu Ala His Asn Asn Val Gly Gln Ile Ser Ala Arg
 325 330 335
 Ala Ser Leu Ile Val His Ala Pro Pro Asn Phe Thr Lys Arg Pro Ser
 340 345 350

Asn Lys Lys Val Gly Leu Asn Gly Val Val Gln Leu Pro Cys Met Ala
 355 360 365
 Ser Gly Asn Pro Pro Pro Ser Val Phe Trp Thr Lys Glu Gly Val Ser
 370 375 380
 Thr Leu Met Phe Pro Asn Ser Ser His Gly Arg Gln Tyr Val Ala Ala
 385 390 395 400
 Asp Gly Thr Leu Gln Ile Thr Asp Val Arg Gln Glu Asp Glu Gly Tyr
 405 410 415
 Tyr Val Cys Ser Ala Phe Ser Val Val Asp Ser Ser Thr Val Arg Val
 420 425 430
 Phe Leu Gln Val Ser Ser Val Asp Glu Arg Pro Pro Pro Ile Ile Gln
 435 440 445
 Ile Gly Pro Ala Asn Gln Thr Leu Pro Lys Gly Ser Val Ala Thr Leu
 450 455 460
 Pro Cys Arg Ala Thr Gly Asn Pro Ser Pro Arg Ile Lys Trp Phe His
 465 470 475 480
 Asp Gly His Ala Val Gln Ala Gly Asn Arg Tyr Ser Ile Ile Gln Gly
 485 490 495
 Ser Ser Leu Arg Val Asp Asp Leu Gln Leu Ser Asp Ser Gly Thr Tyr
 500 505 510
 Thr Cys Ile Ala Ser Gly Glu Arg Gly Glu Thr Ser Trp Ala Ala Thr
 515 520 525
 Leu Thr Val Glu Lys Pro Gly Ser Thr Ser Leu His Arg Ala Ala Asp
 530 535 540
 Pro Ser Thr Tyr Pro Ala Pro Pro Gly Thr Pro Lys Val Leu Asn Val
 545 550 555 560
 Ser Arg Thr Ser Ile Ser Leu Arg Trp Ala Lys Ser Gln Glu Lys Pro
 565 570 575
 Gly Ala Val Gly Pro Ile Ile Gly Tyr Thr Val Glu Tyr Phe Ser Pro
 580 585 590
 Asp Leu Gln Thr Gly Trp Ile Val Ala Ala His Arg Val Gly Asp Thr
 595 600 605
 Gln Val Thr Ile Ser Gly Leu Thr Pro Gly Thr Ser Tyr Val Phe Leu
 610 615 620
 Val Arg Ala Glu Asn Thr Gln Gly Ile Ser Val Pro Ser Gly Leu Ser
 625 630 635 640
 Asn Val Ile Lys Thr Ile Glu Ala Asp Phe Asp Ala Ala Ser Ala Asn
 645 650 655
 Asp Leu Ser Ala Ala Arg Thr Leu Leu Thr Gly Lys Ser Val Glu Leu
 660 665 670

Ile Asp Ala Ser Ala Ile Asn Ala Ser Ala Val Arg Leu Glu Trp Met
 675 680 685
 Leu His Val Ser Ala Asp Glu Lys Tyr Val Glu Gly Leu Arg Ile His
 690 695 700
 Tyr Lys Asp Ala Ser Val Pro Ser Ala Gln Tyr His Ser Ile Thr Val
 705 710 715 720
 Met Asp Ala Ser Ala Glu Ser Phe Val Val Gly Asn Leu Lys Lys Tyr
 725 730 735
 Thr Lys Tyr Glu Phe Phe Leu Thr Pro Phe Phe Glu Thr Ile Glu Gly
 740 745 750
 Gln Pro Ser Asn Ser Lys Thr Ala Leu Thr Tyr Glu Asp Val Pro Ser
 755 760 765
 Ala Pro Pro Asp Asn Ile Gln Ile Gly Met Tyr Asn Gln Thr Ala Gly
 770 775 780
 Trp Val Arg Trp Thr Pro Pro Pro Ser Gln His His Asn Gly Asn Leu
 785 790 795 800
 Tyr Gly Tyr Lys Ile Glu Val Ser Ala Gly Asn Thr Met Lys Val Leu
 805 810 815
 Ala Asn Met Thr Leu Asn Ala Thr Thr Thr Ser Val Leu Leu Asn Asn
 820 825 830
 Leu Thr Thr Gly Ala Val Tyr Ser Val Arg Leu Asn Ser Phe Thr Lys
 835 840 845
 Ala Gly Asp Gly Pro Tyr Ser Lys Pro Ile Ser Leu Phe Met Asp Pro
 850 855 860
 Thr His His Val His Pro Pro Arg Ala His Pro Ser Gly Thr His Asp
 865 870 875 880
 Gly Arg His Glu Gly Gln Asp Leu Thr Tyr His Asn Asn Gly Asn Ile
 885 890 895
 Pro Pro Gly Asp Ile Asn Pro Thr Thr His Lys Lys Thr Thr Asp Tyr
 900 905 910
 Leu Ser Gly Pro Trp Leu Met Val Ile Val Cys Ile Val Leu Leu Val
 915 920 925
 Leu Val Ile Ser Ala Ala Ile Ser Met Val Tyr Phe Lys Arg Lys His
 930 935 940
 Gln Met Thr Lys Glu Leu Gly His Leu Ser Val Val Ser Asp Asn Glu
 945 950 955 960
 Ile Thr Ala Leu Asn Ile Asn Ser Lys Glu Ser Leu Trp Ile Asp His
 965 970 975
 His Arg Gly Trp Arg Thr Ala Asp Thr Asp Lys Asp Ser Gly Leu Ser
 980 985 990

Leu Gln Leu Glu Glu His Gly Ser Ser Ala Lys Gln Arg Gly Gly His
 1315 1320 1325

His Arg Arg Arg Ala Pro Val Val Gln Pro Cys Met Glu Ser Glu Asn
 1330 1335 1340

Glu Asn Met Leu Ala Glu Tyr Glu Gln Arg Gln Tyr Thr Ser Asp Cys
 1345 1350 1355 1360

Cys Asn Ser Ser Arg Glu Gly Asp Thr Cys Ser Cys Ser Glu Gly Ser
 1365 1370 1375

Cys Leu Tyr Ala Glu Ala Gly Glu Pro Ala Pro Arg Gln Met Thr Ala
 1380 1385 1390

Lys Asn Thr
 1395

<210> 3

<211> 4146

<212> DNA

<213> *Drosophila melanogaster*

<220>

<223> *Drosophila roundabout (robo) 2 cDNA*

<400> 3

```

ggtgaaaatc cacgcatcat cgagcatccc atggacacga cggtgccaaa aaatgatcca 60
tttacgttta attgccaggc cgagggcaat ccaacaccaa ccattcaatg gtttaaggac 120
ggtcgcgaac tgaagacgga tacgggttcg catcgcataa tgctgcccgc cgggggtcta 180
ttctttctca aggttatcca ctcacgtaga gagagcgatg cgggcactta ctggtgcgag 240
gccaaaaacg agtttggagt ggcacggtec aggaatgcaa cgttgcaagt ggcagttctc 300
cgcgacgaat tccgtttgga gccggcaaat acccgcggtg cccaaggcga ggtggccctg 360
atggaatgcg gtgccccccg aggatctccg gagccgcaaa tctcgtggcg caagaacggc 420
cagaccctga atcttgtcgg gaacaagcgg attcgcattg tcgacgggtg caatctggcc 480
atccaggaag cccgccaatc ggacgacgga cgctaccagt gtgtggtcaa gaatgtggtt 540
ggcaccocgg agtcggccac cgcttttctt aaagtgcatt tacgtccatt cctcatccga 600
ggaccccaga atcagacggc ggtggtgggc agctcgggtg tcttccagtg ccgcatccga 660
ggcgatcccc tgctgatgtt cctgtggcga cgactgcct cggcgcgcaa tatgccactg 720
cgtaagtttt cttggcttca ttcagcttca ggtcgtgtgc acgtacttga ggaccgcagt 780
ctgaagctcg acgacgttac tctggaggac atgggcgagt acacttgcca ggcggacaat 840
gcggtggggc gcatacggc cactggcatt ctcaccgttc acgctcccc caaatttgtg 900
atacgcacca agaatcagct ggtggagatc ggtgatgaag tgctgttcga gtgccaaagc 960
aatggacatc cccgaccaac gctctactgg tcggtggagg gcaacagctc cctgctgctc 1020
cccggctatc gggatggccg catggaagtg accctgacgc ccgaggggcg ctcggtgctc 1080
tcgatagctc gatttgcccg tgaggattcc ggaaaggtgg tcacttgcaa cgccctgaac 1140
gccgtgggca gcgtcagcag tcggactgtg gtcagtgtgg atacgcaatt cgagctgcca 1200
ccgccgatta tcgaacaggg gcccgatgaat caaacgttgc ccgttaaate aattgtggtt 1260
ctgccatgcc gaactctggg cactccagtg ccacaggtct cttggtacct ggatggcata 1320
cccacgatg tgacaggaga cgagcggcgg aatctttcgg acgctggagc cttaccatt 1380
tcgatcttc agcgccacga ggatgaaggc ttgtacacct gcgtggccag caatcgcaac 1440
ggaaaaatc cttggagtgg ttaccttcgt ctggacaccc cgacaaatcc gaatatcaag 1500
ttcttcagag cccagaaact ttccacctac ccagggccgc caggaaaacc gcaaatggtg 1560
gagaagggcg aaaattcggg gactctcagc tggacgagga gcaacaaggt gggcggtcc 1620
agtctggtg gctatgtaat cgagatgttt ggcaaaaacg aaacggatgg ctgggtggct 1680
gtgggcacta ggtgcaaaa taccacgttt acccaaacg gtctgctgcc ggggtgtaat 1740
tacttctttc taattcgagc cgagaactcc catggcttat cactgccag tccgatgtcg 1800
gaaccctta cggtgggaac gcgctacttc aatagtgttc tggatctgag cgaggctcgt 1860
gccagtctgc tgtcggaga tgttgtggag ctgagcaacg ccagtgtggt ggactccact 1920
agcatgaaac tcacctggca gatcatcaat ggcaaatagc tcgagggctt ctatgtctat 1980

```

Glu Ser Lys Leu Leu Ser His Val Asn Ser Ser Gln Ser Asn Tyr Asn
 995 1000 1005
 Asn Ser Asp Gly Gly Thr Asp Tyr Ala Glu Val Asp Thr Arg Asn Leu
 1010 1015 1020
 Thr Thr Phe Tyr Asn Cys Arg Lys Ser Pro Asp Asn Pro Thr Pro Tyr
 1025 1030 1035 1040
 Ala Thr Thr Met Ile Ile Gly Thr Ser Ser Ser Glu Thr Cys Thr Lys
 1045 1050 1055
 Thr Thr Ser Ile Ser Ala Asp Lys Asp Ser Gly Thr His Ser Pro Tyr
 1060 1065 1070
 Ser Asp Ala Phe Ala Gly Gln Val Pro Ala Val Pro Val Val Lys Ser
 1075 1080 1085
 Asn Tyr Leu Gln Tyr Pro Val Glu Pro Ile Asn Trp Ser Glu Phe Leu
 1090 1095 1100
 Pro Pro Pro Pro Glu His Pro Pro Pro Ser Ser Thr Tyr Gly Tyr Ala
 1105 1110 1115 1120
 Gln Gly Ser Pro Glu Ser Ser Arg Lys Ser Ser Lys Ser Ala Gly Ser
 1125 1130 1135
 Gly Ile Ser Thr Asn Gln Ser Ile Leu Asn Ala Ser Ile His Ser Ser
 1140 1145 1150
 Ser Ser Gly Gly Phe Ser Ala Trp Gly Val Ser Pro Gln Tyr Ala Val
 1155 1160 1165
 Ala Cys Pro Pro Glu Asn Val Tyr Ser Asn Pro Leu Ser Ala Val Ala
 1170 1175 1180
 Gly Gly Thr Gln Asn Arg Tyr Gln Ile Thr Pro Thr Asn Gln His Pro
 1185 1190 1195 1200
 Pro Gln Leu Pro Ala Tyr Phe Ala Thr Thr Gly Pro Gly Gly Ala Val
 1205 1210 1215
 Pro Pro Asn His Leu Pro Phe Ala Thr Gln Arg His Ala Ala Ser Glu
 1220 1225 1230
 Tyr Gln Ala Gly Leu Asn Ala Ala Arg Cys Ala Gln Ser Arg Ala Cys
 1235 1240 1245
 Asn Ser Cys Asp Ala Leu Ala Thr Pro Ser Pro Met Gln Pro Pro Pro
 1250 1255 1260
 Pro Val Pro Val Pro Glu Gly Trp Tyr Gln Pro Val His Pro Asn Ser
 1265 1270 1275 1280
 His Pro Met His Pro Thr Ser Ser Asn His Gln Ile Tyr Gln Cys Ser
 1285 1290 1295
 Ser Glu Cys Ser Asp His Ser Arg Ser Ser Gln Ser His Lys Arg Gln
 1300 1305 1310

```

gcgagacagt tgccaaatcc aatagtc AACATCCGGCGC ccgttactag caataccaat 2040
ccgctgctgg gctctacatc cacatccgca tccgcatccg cctcggcatc ggcattgatt 2100
tcgacaaaagc caaatattgc agctgccggc aaacgtgatg gggagacaaa ccagagtggg 2160
ggaggagctc cgacccact gaacaccaag tatcgcatgc taacgattct caatggcggt 2220
ggcgccatcat cctgcacat caccgggctc gtccagtaca cgctgtatga atttttcatc 2280
gtgccatttt acaaatccgt cgagggcaag ccgtcgaatt cgcgcatcgc tcgcaccctt 2340
gaagatgttc cctctgaggc accatatgga atggaggctc tgctgttgaa ctctcccgcg 2400
gtcttcctca aatggaaggc accagaactc aaggatcggc atggtgttct cttgaactat 2460
catgttatag tccgaggtat tgacactgcc cacaatttct cacgcatttt gacaaatgtc 2520
accatcgatg ccgcttcgcc tactctgggt ttggccaatc tcaccgaagg cgtcatgtac 2580
accgtggggc tgggggccgg aaataacgct ggagttggtc cttatttgtt cccagctact 2640
ttgcgttttg atcccatcac aaagcgactc gatccgttca tcaatcagcg ggaccatgtt 2700
aacgatgtgc tgacgcagcc ctggttcata atactcctgg gcgccatcct ggccgttctt 2760
atgctgtcct ttggcgcaat ggtctttgtg aagcgcaagc acatgatgat gaagcagtcg 2820
gccctaaata caatgcgtgg caatcacacg agcgacgtgc tcaaaatgcc gagtctatcg 2880
gcgcgcaatg gaaacggcta ctggctggac tcctccaccg gcggaatggg gtggcgctcc 2940
tcgcccggcg gcgactcgct ggagatgcaa aaggatcaca tcgccgacta tgcgccggtc 3000
tgccgtgccc ccggttctcc ggccggcggt ggcacctctt ccggtggatc cgggtggcgcg 3060
ggcagcggtg ccagcggcgg cgatgacatt catggaggac acggcagcga acgcaatcag 3120
cagcggtacg tgggcgagta ctccaacata ccgaccgact atgcagaggt gtccagtttt 3180
ggcaaggcac ccagcgagta tggtcggcat ggcaacgcct ccccgcccc ttatgccacc 3240
tcttcgatcc tgagtcccc ccagcagcaa cagcagcagc agccgcgtta tcaacagcga 3300
ccagtgcctg gctatgggct ccagcgccca atgcaccac actaccagca gcagcagcat 3360
cagcagcaac aggcgcagca gacgcaccag caacaccagg ctctccagca gcaccagcaa 3420
ctgccaccga gcaacatcta ccagcagatg tccaccacca gcgagatata cccacgaac 3480
acgggtcctt cgcgctctgt ctactctgag cagtattact accccaagga caagcagaga 3540
cacatccaca tcaccgagaa caagctgagc aactgccaca cctatgaggc ggctcctggc 3600
gccaagcagt cctcgccgat atcctcgag ttccgccagc tgaggcgga gcagctgccg 3660
cccaactgca gcatcggcag ggaaagtgcc cgcttcaagg tgctaaacac ggatcagggc 3720
aagaaccagc agaatctcct ggatctcgac ggctcctcga tgtgctacaa cgggtctggc 3780
gactcgggct gcggtggatc tccctccccg atggccatgc tgatgtcgca cgaggacgag 3840
cacgcgtgtg accacagcgc ggatggggat ctggacgaca tggaacgact gtacgtcaag 3900
gtggacgagc agcagcctcc acagcagcag cagcagctga ttcccctggg ccacagcat 3960
ccggcggaag gtcacctgca gtcctggcgg aatcagagca cgcgagcag tcggaagaac 4020
ggccaggaat gcatcaagga acccagcgag ttgatctacg ctccgggaag cgtggccagc 4080
gaacggagcc tcctcagcaa ctccgggtagc ggcaccagca gccagccagc tggccacaat 4140
gtctga

```

```

<210> 4
<211> 1381
<212> PRT
<213> Drosophila melanogaster

<220>
<223> Drosophila roundabout (robo) 2 protein

```

```

<400> 4
Gly Glu Asn Pro Arg Ile Ile Glu His Pro Met Asp Thr Thr Val Pro
 1                      5                      10                      15

Lys Asn Asp Pro Phe Thr Phe Asn Cys Gln Ala Glu Gly Asn Pro Thr
 20                      25                      30

Pro Thr Ile Gln Trp Phe Lys Asp Gly Arg Glu Leu Lys Thr Asp Thr
 35                      40                      45

Gly Ser His Arg Ile Met Leu Pro Ala Gly Gly Leu Phe Phe Leu Lys
 50                      55                      60

```


Val	Ile	His	Ser	Arg	Arg	Glu	Ser	Asp	Ala	Gly	Thr	Tyr	Trp	Cys	Glu	65	70	75	80
Ala	Lys	Asn	Glu	Phe	Gly	Val	Ala	Arg	Ser	Arg	Asn	Ala	Thr	Leu	Gln	85	90	95	
Val	Ala	Val	Leu	Arg	Asp	Glu	Phe	Arg	Leu	Glu	Pro	Ala	Asn	Thr	Arg	100	105	110	
Val	Ala	Gln	Gly	Glu	Val	Ala	Leu	Met	Glu	Cys	Gly	Ala	Pro	Arg	Gly	115	120	125	
Ser	Pro	Glu	Pro	Gln	Ile	Ser	Trp	Arg	Lys	Asn	Gly	Gln	Thr	Leu	Asn	130	135	140	
Leu	Val	Gly	Asn	Lys	Arg	Ile	Arg	Ile	Val	Asp	Gly	Gly	Asn	Leu	Ala	145	150	155	160
Ile	Gln	Glu	Ala	Arg	Gln	Ser	Asp	Asp	Gly	Arg	Tyr	Gln	Cys	Val	Val	165	170	175	
Lys	Asn	Val	Val	Gly	Thr	Arg	Glu	Ser	Ala	Thr	Ala	Phe	Leu	Lys	Val	180	185	190	
His	Val	Arg	Pro	Phe	Leu	Ile	Arg	Gly	Pro	Gln	Asn	Gln	Thr	Ala	Val	195	200	205	
Val	Gly	Ser	Ser	Val	Val	Phe	Gln	Cys	Arg	Ile	Gly	Gly	Asp	Pro	Leu	210	215	220	
Pro	Asp	Val	Leu	Trp	Arg	Arg	Thr	Ala	Ser	Gly	Gly	Asn	Met	Pro	Leu	225	230	235	240
Arg	Lys	Phe	Ser	Trp	Leu	His	Ser	Ala	Ser	Gly	Arg	Val	His	Val	Leu	245	250	255	
Glu	Asp	Arg	Ser	Leu	Lys	Leu	Asp	Asp	Val	Thr	Leu	Glu	Asp	Met	Gly	260	265	270	
Glu	Tyr	Thr	Cys	Glu	Ala	Asp	Asn	Ala	Val	Gly	Gly	Ile	Thr	Ala	Thr	275	280	285	
Gly	Ile	Leu	Thr	Val	His	Ala	Pro	Pro	Lys	Phe	Val	Ile	Arg	Pro	Lys	290	295	300	
Asn	Gln	Leu	Val	Glu	Ile	Gly	Asp	Glu	Val	Leu	Phe	Glu	Cys	Gln	Ala	305	310	315	320
Asn	Gly	His	Pro	Arg	Pro	Thr	Leu	Tyr	Trp	Ser	Val	Glu	Gly	Asn	Ser	325	330	335	
Ser	Leu	Leu	Leu	Pro	Gly	Tyr	Arg	Asp	Gly	Arg	Met	Glu	Val	Thr	Leu	340	345	350	
Thr	Pro	Glu	Gly	Arg	Ser	Val	Leu	Ser	Ile	Ala	Arg	Phe	Ala	Arg	Glu	355	360	365	
Asp	Ser	Gly	Lys	Val	Val	Thr	Cys	Asn	Ala	Leu	Asn	Ala	Val	Gly	Ser	370	375	380	

Val	Ser	Ser	Arg	Thr	Val	Val	Ser	Val	Asp	Thr	Gln	Phe	Glu	Leu	Pro	385	390	395	400
Pro	Pro	Ile	Ile	Glu	Gln	Gly	Pro	Val	Asn	Gln	Thr	Leu	Pro	Val	Lys		405	410	415
Ser	Ile	Val	Val	Leu	Pro	Cys	Arg	Thr	Leu	Gly	Thr	Pro	Val	Pro	Gln		420	425	430
Val	Ser	Trp	Tyr	Leu	Asp	Gly	Ile	Pro	Ile	Asp	Val	Gln	Glu	His	Glu		435	440	445
Arg	Arg	Asn	Leu	Ser	Asp	Ala	Gly	Ala	Leu	Thr	Ile	Ser	Asp	Leu	Gln		450	455	460
Arg	His	Glu	Asp	Glu	Gly	Leu	Tyr	Thr	Cys	Val	Ala	Ser	Asn	Arg	Asn		465	470	475
Gly	Lys	Ser	Ser	Trp	Ser	Gly	Tyr	Leu	Arg	Leu	Asp	Thr	Pro	Thr	Asn		485	490	495
Pro	Asn	Ile	Lys	Phe	Phe	Arg	Ala	Pro	Glu	Leu	Ser	Thr	Tyr	Pro	Gly		500	505	510
Pro	Pro	Gly	Lys	Pro	Gln	Met	Val	Glu	Lys	Gly	Glu	Asn	Ser	Val	Thr		515	520	525
Leu	Ser	Trp	Thr	Arg	Ser	Asn	Lys	Val	Gly	Gly	Ser	Ser	Leu	Val	Gly		530	535	540
Tyr	Val	Ile	Glu	Met	Phe	Gly	Lys	Asn	Glu	Thr	Asp	Gly	Trp	Val	Ala		545	550	555
Val	Gly	Thr	Arg	Val	Gln	Asn	Thr	Thr	Phe	Thr	Gln	Thr	Gly	Leu	Leu		565	570	575
Pro	Gly	Val	Asn	Tyr	Phe	Phe	Leu	Ile	Arg	Ala	Glu	Asn	Ser	His	Gly		580	585	590
Leu	Ser	Leu	Pro	Ser	Pro	Met	Ser	Glu	Pro	Ile	Thr	Val	Gly	Thr	Arg		595	600	605
Tyr	Phe	Asn	Ser	Gly	Leu	Asp	Leu	Ser	Glu	Ala	Arg	Ala	Ser	Leu	Leu		610	615	620
Ser	Gly	Asp	Val	Val	Glu	Leu	Ser	Asn	Ala	Ser	Val	Val	Asp	Ser	Thr		625	630	635
Ser	Met	Lys	Leu	Thr	Trp	Gln	Ile	Ile	Asn	Gly	Lys	Tyr	Val	Glu	Gly		645	650	655
Phe	Tyr	Val	Tyr	Ala	Arg	Gln	Leu	Pro	Asn	Pro	Ile	Val	Asn	Asn	Pro		660	665	670
Ala	Pro	Val	Thr	Ser	Asn	Thr	Asn	Pro	Leu	Leu	Gly	Ser	Thr	Ser	Thr		675	680	685
Ser	Ala	Ser	Ala	Ser	Ala	Ser	Ala	Ser	Ala	Leu	Ile	Ser	Thr	Lys	Pro		690	695	700

Asn Ile Ala Ala Ala Gly Lys Arg Asp Gly Glu Thr Asn Gln Ser Gly
 705 710 715 720
 Gly Gly Ala Pro Thr Pro Leu Asn Thr Lys Tyr Arg Met Leu Thr Ile
 725 730 735
 Leu Asn Gly Gly Gly Ala Ser Ser Cys Thr Ile Thr Gly Leu Val Gln
 740 745 750
 Tyr Thr Leu Tyr Glu Phe Phe Ile Val Pro Phe Tyr Lys Ser Val Glu
 755 760 765
 Gly Lys Pro Ser Asn Ser Arg Ile Ala Arg Thr Leu Glu Asp Val Pro
 770 775 780
 Ser Glu Ala Pro Tyr Gly Met Glu Ala Leu Leu Leu Asn Ser Ser Ala
 785 790 795 800
 Val Phe Leu Lys Trp Lys Ala Pro Glu Leu Lys Asp Arg His Gly Val
 805 810 815
 Leu Leu Asn Tyr His Val Ile Val Arg Gly Ile Asp Thr Ala His Asn
 820 825 830
 Phe Ser Arg Ile Leu Thr Asn Val Thr Ile Asp Ala Ala Ser Pro Thr
 835 840 845
 Leu Val Leu Ala Asn Leu Thr Glu Gly Val Met Tyr Thr Val Gly Val
 850 855 860
 Ala Ala Gly Asn Asn Ala Gly Val Gly Pro Tyr Cys Val Pro Ala Thr
 865 870 875 880
 Leu Arg Leu Asp Pro Ile Thr Lys Arg Leu Asp Pro Phe Ile Asn Gln
 885 890 895
 Arg Asp His Val Asn Asp Val Leu Thr Gln Pro Trp Phe Ile Ile Leu
 900 905 910
 Leu Gly Ala Ile Leu Ala Val Leu Met Leu Ser Phe Gly Ala Met Val
 915 920 925
 Phe Val Lys Arg Lys His Met Met Met Lys Gln Ser Ala Leu Asn Thr
 930 935 940
 Met Arg Gly Asn His Thr Ser Asp Val Leu Lys Met Pro Ser Leu Ser
 945 950 955 960
 Ala Arg Asn Gly Asn Gly Tyr Trp Leu Asp Ser Ser Thr Gly Gly Met
 965 970 975
 Val Trp Arg Pro Ser Pro Gly Gly Asp Ser Leu Glu Met Gln Lys Asp
 980 985 990
 His Ile Ala Asp Tyr Ala Pro Val Cys Gly Ala Pro Gly Ser Pro Ala
 995 1000 1005
 Gly Gly Gly Thr Ser Ser Gly Gly Ser Gly Gly Ala Gly Ser Gly Ala
 1010 1015 1020

Ser Gly Gly Asp Asp Ile His Gly Gly His Gly Ser Glu Arg Asn Gln
 1025 1030 1035 1040
 Gln Arg Tyr Val Gly Glu Tyr Ser Asn Ile Pro Thr Asp Tyr Ala Glu
 1045 1050 1055
 Val Ser Ser Phe Gly Lys Ala Pro Ser Glu Tyr Gly Arg His Gly Asn
 1060 1065 1070
 Ala Ser Pro Ala Pro Tyr Ala Thr Ser Ser Ile Leu Ser Pro His Gln
 1075 1080 1085
 Gln Gln Gln Gln Gln Gln Pro Arg Tyr Gln Gln Arg Pro Val Pro Gly
 1090 1095 1100
 Tyr Gly Leu Gln Arg Pro Met His Pro His Tyr Gln Gln Gln Gln His
 1105 1110 1115 1120
 Gln Gln Gln Gln Ala Gln Gln Thr His Gln Gln His Gln Ala Leu Gln
 1125 1130 1135
 Gln His Gln Gln Leu Pro Pro Ser Asn Ile Tyr Gln Gln Met Ser Thr
 1140 1145 1150
 Thr Ser Glu Ile Tyr Pro Thr Asn Thr Gly Pro Ser Arg Ser Val Tyr
 1155 1160 1165
 Ser Glu Gln Tyr Tyr Tyr Pro Lys Asp Lys Gln Arg His Ile His Ile
 1170 1175 1180
 Thr Glu Asn Lys Leu Ser Asn Cys His Thr Tyr Glu Ala Ala Pro Gly
 1185 1190 1195 1200
 Ala Lys Gln Ser Ser Pro Ile Ser Ser Gln Phe Ala Ser Val Arg Arg
 1205 1210 1215
 Gln Gln Leu Pro Pro Asn Cys Ser Ile Gly Arg Glu Ser Ala Arg Phe
 1220 1225 1230
 Lys Val Leu Asn Thr Asp Gln Gly Lys Asn Gln Gln Asn Leu Leu Asp
 1235 1240 1245
 Leu Asp Gly Ser Ser Met Cys Tyr Asn Gly Leu Ala Asp Ser Gly Cys
 1250 1255 1260
 Gly Gly Ser Pro Ser Pro Met Ala Met Leu Met Ser His Glu Asp Glu
 1265 1270 1275 1280
 His Ala Leu Tyr His Thr Ala Asp Gly Asp Leu Asp Asp Met Glu Arg
 1285 1290 1295
 Leu Tyr Val Lys Val Asp Glu Gln Gln Pro Pro Gln Gln Gln Gln Gln
 1300 1305 1310
 Leu Ile Pro Leu Val Pro Gln His Pro Ala Glu Gly His Leu Gln Ser
 1315 1320 1325
 Trp Arg Asn Gln Ser Thr Arg Ser Ser Arg Lys Asn Gly Gln Glu Cys
 1330 1335 1340

Ile Lys Glu Pro Ser Glu Leu Ile Tyr Ala Pro Gly Ser Val Ala Ser
 1345 1350 1355 1360

Glu Arg Ser Leu Leu Ser Asn Ser Gly Ser Gly Thr Ser Ser Gln Pro
 1365 1370 1375

Ala Gly His Asn Val
 1380

<210> 5
 <211> 3894
 <212> DNA
 <213> *Caenorhabditis elegans*

<220>
 <223> *C. elegans* roundabout (robo) cDNA

<400> 5
 atgtactatc taggttttta ccacactcac acacacacac acacatacat aaatttttgat 60
 aaaattccta atgcctcaaa tctcgctccc gtgataatcg aacatcccat cgatgtggtg 120
 gtatctaggg gatcgccagc aacctcaca tgtggtgcaa agccatctac cgccaaaatc 180
 acatgggtaca aggatggaca gcccgtaatc acgaataagg agcaagtgaag cagccaccgg 240
 attgttctcg acacgggatc cctgtttctt ctgaaagtga atagtggaaa aaacggaaaa 300
 gacagcgaat cgaggagcgt ctattgtgtg gccagcaacg agcacggaga agtgaagtcg 360
 aacgaaggat cgttaaaatt ggcatgctt cgcaagact ttcgagttcg gccagaaca 420
 gttcaggctc ttggtggaga gatggcgtt ctggaatgca gtccgccacg tggattcccg 480
 gagccggttg tgagctggcg gaaagacgac aaagagctcc gaattcaaga catgccacga 540
 tacactctac actctgacgg aaacctcatc attgatccgg tcgatcgaag cgattctggt 600
 acttatcagt gtgttgccaa caacatgggt ggagaacggg tgtccaatcc cgcaagattg 660
 agtgcctttg agaaaccaa gtttgagcaa gaacccaagg acatgacggg cgacgtcggg 720
 gccgcagtgc tgtttgattg tcgtgtgact ggagatcctc aaccacaaat tacgtggaaa 780
 cgcaaaaatg agccgatgcc agttacacgt gcatacattg ccaaggataa tcgggggttg 840
 agaatcgaaa gagttcaacc atcagacgaa ggtgaatacg tttgctatgc acgaaatcca 900
 gcgggaactc ttgaagcatc tgcacatctt cgtgtccagg cacctccatc cttccagaca 960
 aaaccagcag accagtcagt tccagctgga ggcacggcaa cttttgaatg caccttggtc 1020
 ggtcaaccga gtccgccta tttttggagc aagggaaggcc aacaggatct tcttttcca 1080
 agttatgtgt ccgctgatgg tagaacgaaa gtttcaccaa ctggaacatt gacaattgag 1140
 gaagttcgtc aagttgatga gggagcttat gtgtgcgctg gaatgaactc ggcagggaagc 1200
 tcgttgagca aggcagcttt gaaagcaaca tttgaaacca aaggccgtgt ccaaaaaaaaa 1260
 aagagcaaaa tgggcaaaa gaaacaaaaa aatgttcaat caattatcaa atatttaatt 1320
 tcagccgtga ccggaacac acccgcaaaa ccaccaccaa caatcgagca tggatcatca 1380
 aatcagaccc ttatggttg atcatcagcc atccttccat gtcaggctag cggaaaaacca 1440
 actccaggaa tatcatggct cagggatggg ctacctattg acattacaga tagtcgtatc 1500
 agtcaacatt caacgggaag tctacatatt gccgatttaa agaaacctga caccggagtt 1560
 tacacttgca ttgcgaagaa cgaggatgga gagtcaacat ggtcggcatc tctgactgtt 1620
 gaagatcaca ctagcaatgc acaatttggt cggatgccgg atccatcgaa cttcccgtct 1680
 tctccaacgc aaccattat tgtcaatgtc actgataccg aagtagagct ccaactggaat 1740
 gctccctcca catctggcgc aggaaccaatc actggttata tcattcagta ctacagtcca 1800
 gacctcggag agacgtggtt taacattcca gactacgttg catctactga atatagaata 1860
 aagggtctga aaccatctca ctcttatatg tttgtgattc gagcagaaaa tgagaagggt 1920
 attggaacgc cgagtgtgtc gtcggctctc gttaccacta gcaagccagc agtcaaagtt 1980
 gcgctttctg acaagaacaa aatggacatg gccatcgctg agaagagact cacttcggaa 2040
 caactcataa aactcgagga agtgaagact attaattcta cggccgttcg tttgttctgg 2100
 aagaagagga aacttgaaga gctgattgat gggtactaca tcaagtggag agggcctcca 2160
 agaaccaatg ataataata cgtgaatgtg accagcccta gcaccgaaaa ctatgttggt 2220
 tcaaatttaa tgccattcac caactatgag tttttcgtga ttccttatca ttccggagtt 2280
 catagtattc atggagcacc gagtaattcc atggacgtgt tgaccgccga agctccacct 2340
 tcattgccac cagagatgt gcgaatccgt atgtcaacc tgaccactct tcgtatctct 2400
 tggaaagcac caaaagccga cggcatcaac ggaattctca aaggattcca aattgttatt 2460
 gtttgtcaag cgccaacaa caatcggaac atcactacaa acgagagagc tgccagtgtt 2520

```

actctgttcc atttagtgac tggaaatgacg tataaaatcc gtgtagcggc tagaagcaat 2580
ggtggagttg gagtctcaca tggaaacgagt gaagtcacat tgaatcaaga cacgctggaa 2640
aaacaccttg ctgctcaaca agaaaacgaa tcatttttgt atgggctgat caataaatct 2700
catgttcctg tgattgtcat tgttgcaatt ctgattatct tcgtagtcac cattatagcc 2760
tattgttact ggaggaatag cagaaacagt gatggaaagg atcgaagttt tataaagatc 2820
aatgatggaa gtgttcatat ggcttcgaat aatctttggg atgttgacac aaatccgaat 2880
cagaatccaa tgtacaacac tgctggaaga atgactatga acaatagaaa tggccaggct 2940
ctctattcgc tgacaccaa tgcgcaagac tttttcaaca attgtgatga ctacagtggg 3000
acgatgcaca gaccaggatc cgagcatcac tatcattatg ctcaactgac tggcggacct 3060
ggtaatgcga tgtctacttt ttatggaaac caatatcacg atgatccatc tccatatgcc 3120
accacaacac tggctcctgtc gaaccaacaa ccagcttggc tcaatgacaa aatgcttcgc 3180
gcgcccagaa tgccaacaaa tcccgtgcc cagagccac cggcgcgata tgcagatcat 3240
accgctggaa gacgatctcg atcgagccgt gcattccgat ggagaggaa tctgaatggc 3300
ggactccatc accggactag cggaagtcaa cggctcggata gtccacctca cacagatgtg 3360
agctatgttc agcttcactc atccgatgga actggtagta gtaaggaaa aactggggag 3420
cggagaacac caccgaataa gactctgatg gactttatc cgccaccacc ttccaatcca 3480
ccaccacctg gagggcacgt ttatgacaca gcaactaggc gtcagttgaa tcgtggaagt 3540
actccacgag aagacaccta cgattcgggtc agtgacggag cttttgctcg ggttgatgtg 3600
aatgcaaggc caacgagtcg gaatcggaat ttgggaggaa ggccgctgaa agggaaacga 3660
gacgacgata gtcagcggtc ttcggtgatg atggacgatg atggtggatc ttctgaagct 3720
gacggggaga actctgaagg agacgttccg cgtggagggt ttagaaaagc agttcctcga 3780
atgggtatct ctgcaagtac gctggctcat agttgttacg ggacaaacgg cactgctcaa 3840
cgattccggt caattccacg taacaatgga atcgtcacac aagaacaaac ttga 3894

```

```

<210> 6
<211> 1297
<212> PRT
<213> Caenorhabditis elegans

```

```

<220>
<223> C. elegans roundabout (robo) protein

```

```

<400> 6
Met Tyr Tyr Leu Gly Phe Tyr His Thr His Thr His Thr His Thr Tyr
  1                      5                      10                      15

Ile Asn Phe Asp Lys Ile Pro Asn Ala Ser Asn Leu Ala Pro Val Ile
      20                      25                      30

Ile Glu His Pro Ile Asp Val Val Val Ser Arg Gly Ser Pro Ala Thr
      35                      40                      45

Leu Asn Cys Gly Ala Lys Pro Ser Thr Ala Lys Ile Thr Trp Tyr Lys
      50                      55                      60

Asp Gly Gln Pro Val Ile Thr Asn Lys Glu Gln Val Asn Ser His Arg
      65                      70                      75                      80

Ile Val Leu Asp Thr Gly Ser Leu Phe Leu Leu Lys Val Asn Ser Gly
      85                      90                      95

Lys Asn Gly Lys Asp Ser Asp Ala Gly Ala Tyr Tyr Cys Val Ala Ser
      100                      105                      110

Asn Glu His Gly Glu Val Lys Ser Asn Glu Gly Ser Leu Lys Leu Ala
      115                      120                      125

Met Leu Arg Glu Asp Phe Arg Val Arg Pro Arg Thr Val Gln Ala Leu
      130                      135                      140

```

Gly	Gly	Glu	Met	Ala	Val	Leu	Glu	Cys	Ser	Pro	Pro	Arg	Gly	Phe	Pro	145	150	155	160
Glu	Pro	Val	Val	Ser	Trp	Arg	Lys	Asp	Asp	Lys	Glu	Leu	Arg	Ile	Gln	165	170	175	
Asp	Met	Pro	Arg	Tyr	Thr	Leu	His	Ser	Asp	Gly	Asn	Leu	Ile	Ile	Asp	180	185	190	
Pro	Val	Asp	Arg	Ser	Asp	Ser	Gly	Thr	Tyr	Gln	Cys	Val	Ala	Asn	Asn	195	200	205	
Met	Val	Gly	Glu	Arg	Val	Ser	Asn	Pro	Ala	Arg	Leu	Ser	Val	Phe	Glu	210	215	220	
Lys	Pro	Lys	Phe	Glu	Gln	Glu	Pro	Lys	Asp	Met	Thr	Val	Asp	Val	Gly	225	230	235	240
Ala	Ala	Val	Leu	Phe	Asp	Cys	Arg	Val	Thr	Gly	Asp	Pro	Gln	Pro	Gln	245	250	255	
Ile	Thr	Trp	Lys	Arg	Lys	Asn	Glu	Pro	Met	Pro	Val	Thr	Arg	Ala	Tyr	260	265	270	
Ile	Ala	Lys	Asp	Asn	Arg	Gly	Leu	Arg	Ile	Glu	Arg	Val	Gln	Pro	Ser	275	280	285	
Asp	Glu	Gly	Glu	Tyr	Val	Cys	Tyr	Ala	Arg	Asn	Pro	Ala	Gly	Thr	Leu	290	295	300	
Glu	Ala	Ser	Ala	His	Leu	Arg	Val	Gln	Ala	Pro	Pro	Ser	Phe	Gln	Thr	305	310	315	320
Lys	Pro	Ala	Asp	Gln	Ser	Val	Pro	Ala	Gly	Gly	Thr	Ala	Thr	Phe	Glu	325	330	335	
Cys	Thr	Leu	Val	Gly	Gln	Pro	Ser	Pro	Ala	Tyr	Phe	Trp	Ser	Lys	Glu	340	345	350	
Gly	Gln	Gln	Asp	Leu	Leu	Phe	Pro	Ser	Tyr	Val	Ser	Ala	Asp	Gly	Arg	355	360	365	
Thr	Lys	Val	Ser	Pro	Thr	Gly	Thr	Leu	Thr	Ile	Glu	Glu	Val	Arg	Gln	370	375	380	
Val	Asp	Glu	Gly	Ala	Tyr	Val	Cys	Ala	Gly	Met	Asn	Ser	Ala	Gly	Ser	385	390	395	400
Ser	Leu	Ser	Lys	Ala	Ala	Leu	Lys	Ala	Thr	Phe	Glu	Thr	Lys	Gly	Arg	405	410	415	
Val	Gln	Lys	Lys	Lys	Ser	Lys	Met	Gly	Lys	Gln	Lys	Gln	Lys	Asn	Val	420	425	430	
Gln	Ser	Ile	Ile	Lys	Tyr	Leu	Ile	Ser	Ala	Val	Thr	Gly	Asn	Thr	Pro	435	440	445	
Ala	Lys	Pro	Pro	Pro	Thr	Ile	Glu	His	Gly	His	Gln	Asn	Gln	Thr	Leu	450	455	460	

Met Val Gly Ser Ser Ala Ile Leu Pro Cys Gln Ala Ser Gly Lys Pro
 465 470 475 480
 Thr Pro Gly Ile Ser Trp Leu Arg Asp Gly Leu Pro Ile Asp Ile Thr
 485 490 495
 Asp Ser Arg Ile Ser Gln His Ser Thr Gly Ser Leu His Ile Ala Asp
 500 505 510
 Leu Lys Lys Pro Asp Thr Gly Val Tyr Thr Cys Ile Ala Lys Asn Glu
 515 520 525
 Asp Gly Glu Ser Thr Trp Ser Ala Ser Leu Thr Val Glu Asp His Thr
 530 535 540
 Ser Asn Ala Gln Phe Val Arg Met Pro Asp Pro Ser Asn Phe Pro Ser
 545 550 555 560
 Ser Pro Thr Gln Pro Ile Ile Val Asn Val Thr Asp Thr Glu Val Glu
 565 570 575
 Leu His Trp Asn Ala Pro Ser Thr Ser Gly Ala Gly Pro Ile Thr Gly
 580 585 590
 Tyr Ile Ile Gln Tyr Tyr Ser Pro Asp Leu Gly Gln Thr Trp Phe Asn
 595 600 605
 Ile Pro Asp Tyr Val Ala Ser Thr Glu Tyr Arg Ile Lys Gly Leu Lys
 610 615 620
 Pro Ser His Ser Tyr Met Phe Val Ile Arg Ala Glu Asn Glu Lys Gly
 625 630 635 640
 Ile Gly Thr Pro Ser Val Ser Ser Ala Leu Val Thr Thr Ser Lys Pro
 645 650 655
 Ala Ala Gln Val Ala Leu Ser Asp Lys Asn Lys Met Asp Met Ala Ile
 660 665 670
 Ala Glu Lys Arg Leu Thr Ser Glu Gln Leu Ile Lys Leu Glu Glu Val
 675 680 685
 Lys Thr Ile Asn Ser Thr Ala Val Arg Leu Phe Trp Lys Lys Arg Lys
 690 695 700
 Leu Glu Glu Leu Ile Asp Gly Tyr Tyr Ile Lys Trp Arg Gly Pro Pro
 705 710 715 720
 Arg Thr Asn Asp Asn Gln Tyr Val Asn Val Thr Ser Pro Ser Thr Glu
 725 730 735
 Asn Tyr Val Val Ser Asn Leu Met Pro Phe Thr Asn Tyr Glu Phe Phe
 740 745 750
 Val Ile Pro Tyr His Ser Gly Val His Ser Ile His Gly Ala Pro Ser
 755 760 765
 Asn Ser Met Asp Val Leu Thr Ala Glu Ala Pro Pro Ser Leu Pro Pro
 770 775 780

Glu	Asp	Val	Arg	Ile	Arg	Met	Leu	Asn	Leu	Thr	Thr	Leu	Arg	Ile	Ser	785	790	795	800
Trp	Lys	Ala	Pro	Lys	Ala	Asp	Gly	Ile	Asn	Gly	Ile	Leu	Lys	Gly	Phe	805	810		815
Gln	Ile	Val	Ile	Val	Gly	Gln	Ala	Pro	Asn	Asn	Asn	Arg	Asn	Ile	Thr	820	825		830
Thr	Asn	Glu	Arg	Ala	Ala	Ser	Val	Thr	Leu	Phe	His	Leu	Val	Thr	Gly	835	840		845
Met	Thr	Tyr	Lys	Ile	Arg	Val	Ala	Ala	Arg	Ser	Asn	Gly	Gly	Val	Gly	850	855		860
Val	Ser	His	Gly	Thr	Ser	Glu	Val	Ile	Met	Asn	Gln	Asp	Thr	Leu	Glu	865	870		875
Lys	His	Leu	Ala	Ala	Gln	Gln	Glu	Asn	Glu	Ser	Phe	Leu	Tyr	Gly	Leu	885	890		895
Ile	Asn	Lys	Ser	His	Val	Pro	Val	Ile	Val	Ile	Val	Ala	Ile	Leu	Ile	900	905		910
Ile	Phe	Val	Val	Ile	Ile	Ile	Ala	Tyr	Cys	Tyr	Trp	Arg	Asn	Ser	Arg	915	920		925
Asn	Ser	Asp	Gly	Lys	Asp	Arg	Ser	Phe	Ile	Lys	Ile	Asn	Asp	Gly	Ser	930	935		940
Val	His	Met	Ala	Ser	Asn	Asn	Leu	Trp	Asp	Val	Ala	Gln	Asn	Pro	Asn	945	950		955
Gln	Asn	Pro	Met	Tyr	Asn	Thr	Ala	Gly	Arg	Met	Thr	Met	Asn	Asn	Arg	965	970		975
Asn	Gly	Gln	Ala	Leu	Tyr	Ser	Leu	Thr	Pro	Asn	Ala	Gln	Asp	Phe	Phe	980	985		990
Asn	Asn	Cys	Asp	Asp	Tyr	Ser	Gly	Thr	Met	His	Arg	Pro	Gly	Ser	Glu	995	1000		1005
His	His	Tyr	His	Tyr	Ala	Gln	Leu	Thr	Gly	Gly	Pro	Gly	Asn	Ala	Met	1010	1015		1020
Ser	Thr	Phe	Tyr	Gly	Asn	Gln	Tyr	His	Asp	Asp	Pro	Ser	Pro	Tyr	Ala	1025	1030		1035
Thr	Thr	Thr	Leu	Val	Leu	Ser	Asn	Gln	Gln	Pro	Ala	Trp	Leu	Asn	Asp	1045	1050		1055
Lys	Met	Leu	Arg	Ala	Pro	Ala	Met	Pro	Thr	Asn	Pro	Val	Pro	Pro	Glu	1060	1065		1070
Pro	Pro	Ala	Arg	Tyr	Ala	Asp	His	Thr	Ala	Gly	Arg	Arg	Ser	Arg	Ser	1075	1080		1085
Ser	Arg	Ala	Ser	Asp	Gly	Arg	Gly	Thr	Leu	Asn	Gly	Gly	Leu	His	His	1090	1095		1100

Arg Thr Ser Gly Ser Gln Arg Ser Asp Ser Pro Pro His Thr Asp Val
 1105 1110 1115 1120
 Ser Tyr Val Gln Leu His Ser Ser Asp Gly Thr Gly Ser Ser Lys Glu
 1125 1130 1135
 Arg Thr Gly Glu Arg Arg Thr Pro Pro Asn Lys Thr Leu Met Asp Phe
 1140 1145 1150
 Ile Pro Pro Pro Pro Ser Asn Pro Pro Pro Gly Gly His Val Tyr
 1155 1160 1165
 Asp Thr Ala Thr Arg Arg Gln Leu Asn Arg Gly Ser Thr Pro Arg Glu
 1170 1175 1180
 Asp Thr Tyr Asp Ser Val Ser Asp Gly Ala Phe Ala Arg Val Asp Val
 1185 1190 1195 1200
 Asn Ala Arg Pro Thr Ser Arg Asn Arg Asn Leu Gly Gly Arg Pro Leu
 1205 1210 1215
 Lys Gly Lys Arg Asp Asp Asp Ser Gln Arg Ser Ser Leu Met Met Asp
 1220 1225 1230
 Asp Asp Gly Gly Ser Ser Glu Ala Asp Gly Glu Asn Ser Glu Gly Asp
 1235 1240 1245
 Val Pro Arg Gly Gly Val Arg Lys Ala Val Pro Arg Met Gly Ile Ser
 1250 1255 1260
 Ala Ser Thr Leu Ala His Ser Cys Tyr Gly Thr Asn Gly Thr Ala Gln
 1265 1270 1275 1280
 Arg Phe Arg Ser Ile Pro Arg Asn Asn Gly Ile Val Thr Gln Glu Gln
 1285 1290 1295

Thr

<210> 7

<211> 4956

<212> DNA

<213> Homo sapiens

<220>

<223> human roundabout (robo) 1 cDNA

<400> 7

```

atgaaatgga aacatgttcc ttttttggtc atgatatcac tctcagctt atccccaaat 60
cacctgtttc tggcccagct tattccagac cctgaagatg tagagagggg gaacgaccac 120
gggacgcca tccccacctc tgataacgat gacaattcgc tgggctatac aggctcccgt 180
cttcgtcagg aagattttcc acctcgcatt gttgaacacc cttcagacct gattgtctca 240
aaaggagaac ctgcaacttt gaactgcaaa gctgaaggcc gccccacacc cactattgaa 300
tggtacaaag ggggagagag agtggagaca gacaaagatg accctcgctc acaccgaatg 360
ttgctgccga gtggatcttt atttttctta cgtatagtag atggacggaa aagtagacct 420
gatgaaggag tctatgtctg tgtagyaagg aattaccttg gagaggctgt gagccacaat 480
gcatcgctgg aagtagccat acttcgggat gacttcagac aaaacccttc ggatgtcatg 540
gttgtagtag gagagcctgc agtaatggaa tgccaacctc cacgaggcca tctgagccc 600
accatttcat ggaagaaaga tggctctcca ctggatgata aagatgaaag aataactata 660
cgaggaggaa agctcatgat cacttacacc cgtaaaagtg acgctggcaa atatgtttgt 720
gttggtacca atatggttgg ggaacgtgag agtgaagtag ccgagctgac tgtcttagag 780
  
```

agaccatcat	ttgtgaagag	accagtaac	ttggcagtaa	ctgtggatga	cagtgcagaa	840
tttaaagtgt	aggcccagg	tgaccctgta	cctacagtac	gatggaggaa	agatgatgga	900
gagctgcccc	aatccagata	tgaaatccga	gatgatcata	ccttgaaaat	taggaaggtg	960
acagctgggtg	acatgggttc	atacacttgt	gttgacagaaa	atatgggtggg	caaagctgaa	1020
gcattctgcta	ctctgactgt	tcaagaacct	ccacattttt	ttgtgaaacc	ccgtgaccag	1080
gttggttgcct	tgggacggac	tgtaactttt	cagtgtgaag	caaccggaaa	tcctcaacca	1140
gctatttttct	ggaggagaga	agggagtcag	aatctacttt	tctcatatca	accaccacag	1200
tcattccagcc	gattttcagt	ctcccagact	ggcgacctca	caattactaa	tgtccagcga	1260
tctgatgttg	gttattacat	ctgccagact	ttaaatgttg	ctggaagcat	catcacaag	1320
gcataatttgg	aagttacaga	tgtgattgca	gatcggcctc	ccccagttat	tcgacaagg	1380
cctgtgaatc	agactgtagc	cgtggatggc	acttttcgtc	tcagctgtgt	ggccacaggc	1440
agtccagtgc	ccaccattct	gtggagaaag	gatggagtcc	tcgtttcaac	ccaagactct	1500
cgaatcaaac	agttggagaa	tggagtactg	cagatccgat	atgctaagct	gggtgatact	1560
ggtcggtaca	cctgcattgc	atcaaccccc	agtggtgaag	caacatggag	tgtttacatt	1620
gaagttcaag	aatttggagt	tccagttcag	cctccaagac	ctactgaccc	aaattttaatc	1680
cctagtgtccc	catcaaaacc	tgaagtgaca	gatgtcagca	gaaatacagt	cacattatcg	1740
tggcaaccaa	atttgaattc	aggagcaact	ccaacatctt	atattataga	agccttcagc	1800
catgcatctg	gtagcagctg	gcagaccgta	gcagagaatg	tgaaaacaga	aacatctgcc	1860
attaaaggac	tcaaacctaa	tgcaattttac	cttttccttg	tgagggcagc	taatgcatat	1920
ggaattagtg	atccaagcca	aatatcagat	ccagtgaaaa	cacaagatgt	cctaccaaca	1980
agtcaggggg	tggaccacaa	gcagggtccag	agagagctgg	gaaatgctgt	tctgcacctc	2040
cacaacccca	ccgtcttttc	ttcctcttcc	atcgaagtgc	actggacagt	agatcaacag	2100
tctcagtata	tacaaggata	taaaattctc	tatcggccat	ctggagccaa	ccacggagaa	2160
tcagactggt	tagtttttga	agtgaggacg	ccagccaaaa	acagtgtggt	aatccctgat	2220
ctcagaaagg	gagtcaacta	tgaaatttaag	gctcgcctt	tttttaatga	atttcaagga	2280
gcagatagtg	aaatcaagtt	tgccaaaacc	ctggaagaag	cacccagtgc	cccccccaa	2340
ggtgtaactg	tatccaagaa	tgatggaaac	ggaactgcaa	ttctagttag	ttggcagcca	2400
cctccagaag	acactcaaaa	tggaatggtc	caagagtata	aggtttggtg	tctgggcaat	2460
gaaactcgat	accacatcaa	caaaacagtg	gatggttcca	ccttttcctg	ggtcattccc	2520
tttcttggtc	ctggaatccg	atacagtgtg	gaagtggcag	ccagcactgg	ggctgggtct	2580
ggggtaaaga	gtgagcctca	gttcatccag	ctggatgccc	atggaaaacc	tgtgtcacct	2640
gaggaccaag	tcagcctcgc	tcagcagatt	tcagatgtgg	tgaagcagcc	ggccttcata	2700
gcaggtattg	gagcagcctg	ttggatcatc	ctcatgtctc	tcagcatctg	gctttatcga	2760
caccgcaaga	agagaaacgg	acttactagt	acctacgcgg	gtatcagaaa	agtcccgctc	2820
tttaccttca	caccaacagt	aacttaccag	agaggaggcg	aagctgtcag	cagtggaggg	2880
aggcctggac	ttctcaacat	cagtgaacct	gccgcgcagc	catggctggc	agacacgtgg	2940
cctaatactg	gcaacaacca	caatgactgc	tccatcagct	gctgcacggc	aggcaatgga	3000
aacagcgaca	gcaacctcac	tacctacagt	cgcccagctg	attgtatagc	aaattataac	3060
aaccaactgg	ataacaaaca	aacaaatctg	atgctccctg	agtcaactgt	ttatgggtgat	3120
gtggacctta	gtaacaaaat	caatgagatg	aaaaccttca	atagcccaaa	tctgaaggat	3180
gggcgttttg	tcaatccatc	agggcagcct	actccttacg	ccaccactca	gctcatccag	3240
tcaaacctca	gcaacaacat	gaacaatggc	agcggggact	ctggcgagaa	gcactggaaa	3300
ccactgggac	agcagaaaca	agaagtggca	ccagttcagt	acaacatcgt	ggagcaaaaac	3360
aagctgaaca	aagattatcg	agcaaatgac	acagttcctc	caactatccc	atacaaccaa	3420
tcatacgacc	agaacacagg	aggatcctac	aacagctcag	accggggcag	tagtacatct	3480
gggagtcagg	ggcacaagaa	aggggcaaga	acacccaagg	tacaaaaaca	gggtggcatg	3540
aactgggcag	acctgcttcc	tcctccccc	gcacatcctc	ctccacacag	caatagcgaa	3600
gagtacaaca	tttctgtaga	tgaaagctat	gaccaagaaa	tgccatgtcc	cgtgccacca	3660
gcaaggatgt	atttgcaaca	agatgaatta	gaagaggagg	aagatgaacg	aggccccact	3720
ccccctgttc	ggggagcagc	ttcttctcca	gctgccgtgt	cctatagcca	tcagtcact	3780
gccactctga	ctccctcccc	acaggaagaa	ctccagccca	tgttacagga	ttgtccagag	3840
gagactggcc	acatgcagca	ccagcccgac	aggagacggc	agcctgtgag	tcctcctcca	3900
ccaccacggc	cgatctcccc	tccacatacc	tatggctaca	tttcaggacc	cctggtctca	3960
gatatggata	cggatgcgcc	agaagaggaa	gaagacgaag	ccgacatgga	ggtagccaag	4020
atgcaaacca	gaaggctttt	gttacgtggg	cttgagcaga	cacctgcctc	cagtgttggg	4080
gacctggaga	gctctgtcac	ggggtccatg	atcaacggct	ggggctcagc	ctcagaggag	4140
gacaacattt	ccagcggacg	ctccagtgtt	agttcttcgg	acggctcctt	tttcaactgat	4200
gctgactttg	cccaggcagt	cgcagcagcg	gcagagtatg	ctggtctgaa	agtagcacga	4260
cggcaaatgc	aggatctgcg	tggccgtcga	cattttcatg	cgtctcagtg	ccctaggccc	4320
acaagtcocg	tgtctacaga	cagcaacatg	agtgcccgcc	taatgcagaa	aaccagacca	4380
gccaagaaac	tgaaacacca	gccaggacat	ctgcgcagag	aaacctacac	agatgatctt	4440

```

ccaccacctc ctgtgccgcc acctgctata aagtcaccta ctgcccacac 4500
ctggaagtac gacctgtagt ggtgccaaaa ctcccttcta tggatgcaag aacagacaga 4560
tcatcagaca gaaaaggaag cagttacaag gggagagaag tgttgatgg aagacaggtt 4620
gttgacatgc gaacaaatcc aggtgatccc agagaagcac aggaacagca aaatgacggg 4680
aaaggacgtg gaaacaaggc agcaaaaacga gaccttccac cagcaaagac tcatctcatc 4740
caagaggata ttctacctta ttgtagacct acttttccaa catcaaataa tcccagagat 4800
cccagttcct caagctcaat gtcatcaaga ggatcaggaa gcagacaaaag agaacaagca 4860
aatgtaggtc gaagaaatat tgcagaaatg caggtacttg gaggatatga aagaggagaa 4920
gataataatg aagaattaga ggaaactgaa agctga 4956

```

<210> 8

<211> 1651

<212> PRT

<213> Homo sapiens

<220>

<223> human roundabout (robo) 1 (H1) protein

<400> 8

```

Met Lys Trp Lys His Val Pro Phe Leu Val Met Ile Ser Leu Leu Ser
  1              5              10              15

Leu Ser Pro Asn His Leu Phe Leu Ala Gln Leu Ile Pro Asp Pro Glu
          20              25              30

Asp Val Glu Arg Gly Asn Asp His Gly Thr Pro Ile Pro Thr Ser Asp
    35              40              45

Asn Asp Asp Asn Ser Leu Gly Tyr Thr Gly Ser Arg Leu Arg Gln Glu
    50              55              60

Asp Phe Pro Pro Arg Ile Val Glu His Pro Ser Asp Leu Ile Val Ser
    65              70              75              80

Lys Gly Glu Pro Ala Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr
          85              90              95

Pro Thr Ile Glu Trp Tyr Lys Gly Gly Glu Arg Val Glu Thr Asp Lys
    100              105              110

Asp Asp Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe
    115              120              125

Phe Leu Arg Ile Val His Gly Arg Lys Ser Arg Pro Asp Glu Gly Val
    130              135              140

Tyr Val Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser His Asn
    145              150              155              160

Ala Ser Leu Glu Val Ala Ile Leu Arg Asp Asp Phe Arg Gln Asn Pro
    165              170              175

Ser Asp Val Met Val Ala Val Gly Glu Pro Ala Val Met Glu Cys Gln
    180              185              190

Pro Pro Arg Gly His Pro Glu Pro Thr Ile Ser Trp Lys Lys Asp Gly
    195              200              205

Ser Pro Leu Asp Asp Lys Asp Glu Arg Ile Thr Ile Arg Gly Gly Lys
    210              215              220

```

Leu	Met	Ile	Thr	Tyr	Thr	Arg	Lys	Ser	Asp	Ala	Gly	Lys	Tyr	Val	Cys	
225					230					235					240	
Val	Gly	Thr	Asn	Met	Val	Gly	Glu	Arg	Glu	Ser	Glu	Val	Ala	Glu	Leu	
			245						250					255		
Thr	Val	Leu	Glu	Arg	Pro	Ser	Phe	Val	Lys	Arg	Pro	Ser	Asn	Leu	Ala	
			260					265					270			
Val	Thr	Val	Asp	Asp	Ser	Ala	Glu	Phe	Lys	Cys	Glu	Ala	Arg	Gly	Asp	
		275					280					285				
Pro	Val	Pro	Thr	Val	Arg	Trp	Arg	Lys	Asp	Asp	Gly	Glu	Leu	Pro	Lys	
	290					295					300					
Ser	Arg	Tyr	Glu	Ile	Arg	Asp	Asp	His	Thr	Leu	Lys	Ile	Arg	Lys	Val	
305					310					315					320	
Thr	Ala	Gly	Asp	Met	Gly	Ser	Tyr	Thr	Cys	Val	Ala	Glu	Asn	Met	Val	
				325					330					335		
Gly	Lys	Ala	Glu	Ala	Ser	Ala	Thr	Leu	Thr	Val	Gln	Glu	Pro	Pro	His	
			340					345					350			
Phe	Val	Val	Lys	Pro	Arg	Asp	Gln	Val	Val	Ala	Leu	Gly	Arg	Thr	Val	
		355					360					365				
Thr	Phe	Gln	Cys	Glu	Ala	Thr	Gly	Asn	Pro	Gln	Pro	Ala	Ile	Phe	Trp	
	370					375					380					
Arg	Arg	Glu	Gly	Ser	Gln	Asn	Leu	Leu	Phe	Ser	Tyr	Gln	Pro	Pro	Gln	
385					390					395					400	
Ser	Ser	Ser	Arg	Phe	Ser	Val	Ser	Gln	Thr	Gly	Asp	Leu	Thr	Ile	Thr	
				405					410					415		
Asn	Val	Gln	Arg	Ser	Asp	Val	Gly	Tyr	Tyr	Ile	Cys	Gln	Thr	Leu	Asn	
			420					425					430			
Val	Ala	Gly	Ser	Ile	Ile	Thr	Lys	Ala	Tyr	Leu	Glu	Val	Thr	Asp	Val	
		435					440					445				
Ile	Ala	Asp	Arg	Pro	Pro	Pro	Val	Ile	Arg	Gln	Gly	Pro	Val	Asn	Gln	
	450					455					460					
Thr	Val	Ala	Val	Asp	Gly	Thr	Phe	Val	Leu	Ser	Cys	Val	Ala	Thr	Gly	
465					470					475					480	
Ser	Pro	Val	Pro	Thr	Ile	Leu	Trp	Arg	Lys	Asp	Gly	Val	Leu	Val	Ser	
				485					490					495		
Thr	Gln	Asp	Ser	Arg	Ile	Lys	Gln	Leu	Glu	Asn	Gly	Val	Leu	Gln	Ile	
			500					505					510			
Arg	Tyr	Ala	Lys	Leu	Gly	Asp	Thr	Gly	Arg	Tyr	Thr	Cys	Ile	Ala	Ser	
		515					520					525				
Thr	Pro	Ser	Gly	Glu	Ala	Thr	Trp	Ser	Ala	Tyr	Ile	Glu	Val	Gln	Glu	
	530					535					540					

Phe Gly Val Pro Val Gln Pro Pro Arg Pro Thr Asp Pro Asn Leu Ile
545 550 555 560
Pro Ser Ala Pro Ser Lys Pro Glu Val Thr Asp Val Ser Arg Asn Thr
565 570 575
Val Thr Leu Ser Trp Gln Pro Asn Leu Asn Ser Gly Ala Thr Pro Thr
580 585 590
Ser Tyr Ile Ile Glu Ala Phe Ser His Ala Ser Gly Ser Ser Trp Gln
595 600 605
Thr Val Ala Glu Asn Val Lys Thr Glu Thr Ser Ala Ile Lys Gly Leu
610 615 620
Lys Pro Asn Ala Ile Tyr Leu Phe Leu Val Arg Ala Ala Asn Ala Tyr
625 630 635 640
Gly Ile Ser Asp Pro Ser Gln Ile Ser Asp Pro Val Lys Thr Gln Asp
645 650 655
Val Leu Pro Thr Ser Gln Gly Val Asp His Lys Gln Val Gln Arg Glu
660 665 670
Leu Gly Asn Ala Val Leu His Leu His Asn Pro Thr Val Leu Ser Ser
675 680 685
Ser Ser Ile Glu Val His Trp Thr Val Asp Gln Gln Ser Gln Tyr Ile
690 695 700
Gln Gly Tyr Lys Ile Leu Tyr Arg Pro Ser Gly Ala Asn His Gly Glu
705 710 715 720
Ser Asp Trp Leu Val Phe Glu Val Arg Thr Pro Ala Lys Asn Ser Val
725 730 735
Val Ile Pro Asp Ile Arg Lys Gly Val Asn Tyr Glu Ile Lys Ala Arg
740 745 750
Pro Phe Phe Asn Glu Phe Gln Gly Ala Asp Ser Glu Ile Lys Phe Ala
755 760 765
Lys Thr Leu Glu Glu Ala Pro Ser Ala Pro Pro Gln Gly Val Thr Val
770 775 780
Ser Lys Asn Asp Gly Asn Gly Thr Ala Ile Leu Val Ser Trp Gln Pro
785 790 795 800
Pro Pro Glu Asp Thr Gln Asn Gly Met Val Gln Glu Tyr Lys Val Trp
805 810 815
Cys Leu Gly Asn Glu Thr Arg Tyr His Ile Asn Lys Thr Val Asp Gly
820 825 830
Ser Thr Phe Ser Val Val Ile Pro Phe Leu Val Pro Gly Ile Arg Tyr
835 840 845
Ser Val Glu Val Ala Ala Ser Thr Gly Ala Gly Ser Gly Val Lys Ser
850 855 860

Glu	Pro	Gln	Phe	Ile	Gln	Leu	Asp	Ala	His	Gly	Asn	Pro	Val	Ser	Pro	865	870	875	880
Glu	Asp	Gln	Val	Ser	Leu	Ala	Gln	Gln	Ile	Ser	Asp	Val	Val	Lys	Gln	885	890	895	
Pro	Ala	Phe	Ile	Ala	Gly	Ile	Gly	Ala	Ala	Cys	Trp	Ile	Ile	Leu	Met	900	905	910	
Val	Phe	Ser	Ile	Trp	Leu	Tyr	Arg	His	Arg	Lys	Lys	Arg	Asn	Gly	Leu	915	920	925	
Thr	Ser	Thr	Tyr	Ala	Gly	Ile	Arg	Lys	Val	Pro	Ser	Phe	Thr	Phe	Thr	930	935	940	
Pro	Thr	Val	Thr	Tyr	Gln	Arg	Gly	Gly	Glu	Ala	Val	Ser	Ser	Gly	Gly	945	950	955	960
Arg	Pro	Gly	Leu	Leu	Asn	Ile	Ser	Glu	Pro	Ala	Ala	Gln	Pro	Trp	Leu	965	970	975	
Ala	Asp	Thr	Trp	Pro	Asn	Thr	Gly	Asn	Asn	His	Asn	Asp	Cys	Ser	Ile	980	985	990	
Ser	Cys	Cys	Thr	Ala	Gly	Asn	Gly	Asn	Ser	Asp	Ser	Asn	Leu	Thr	Thr	995	1000	1005	
Tyr	Ser	Arg	Pro	Ala	Asp	Cys	Ile	Ala	Asn	Tyr	Asn	Asn	Gln	Leu	Asp	1010	1015	1020	
Asn	Lys	Gln	Thr	Asn	Leu	Met	Leu	Pro	Glu	Ser	Thr	Val	Tyr	Gly	Asp	1025	1030	1035	1040
Val	Asp	Leu	Ser	Asn	Lys	Ile	Asn	Glu	Met	Lys	Thr	Phe	Asn	Ser	Pro	1045	1050	1055	
Asn	Leu	Lys	Asp	Gly	Arg	Phe	Val	Asn	Pro	Ser	Gly	Gln	Pro	Thr	Pro	1060	1065	1070	
Tyr	Ala	Thr	Thr	Gln	Leu	Ile	Gln	Ser	Asn	Leu	Ser	Asn	Asn	Met	Asn	1075	1080	1085	
Asn	Gly	Ser	Gly	Asp	Ser	Gly	Glu	Lys	His	Trp	Lys	Pro	Leu	Gly	Gln	1090	1095	1100	
Gln	Lys	Gln	Glu	Val	Ala	Pro	Val	Gln	Tyr	Asn	Ile	Val	Glu	Gln	Asn	1105	1110	1115	1120
Lys	Leu	Asn	Lys	Asp	Tyr	Arg	Ala	Asn	Asp	Thr	Val	Pro	Pro	Thr	Ile	1125	1130	1135	
Pro	Tyr	Asn	Gln	Ser	Tyr	Asp	Gln	Asn	Thr	Gly	Gly	Ser	Tyr	Asn	Ser	1140	1145	1150	
Ser	Asp	Arg	Gly	Ser	Ser	Thr	Ser	Gly	Ser	Gln	Gly	His	Lys	Lys	Gly	1155	1160	1165	
Ala	Arg	Thr	Pro	Lys	Val	Pro	Lys	Gln	Gly	Gly	Met	Asn	Trp	Ala	Asp	1170	1175	1180	

Leu Leu Pro Pro Pro Pro Ala His Pro Pro Pro His Ser Asn Ser Glu
 1185 1190 1195 1200
 Glu Tyr Asn Ile Ser Val Asp Glu Ser Tyr Asp Gln Glu Met Pro Cys
 1205 1210 1215
 Pro Val Pro Pro Ala Arg Met Tyr Leu Gln Gln Asp Glu Leu Glu Glu
 1220 1225 1230
 Glu Glu Asp Glu Arg Gly Pro Thr Pro Pro Val Arg Gly Ala Ala Ser
 1235 1240 1245
 Ser Pro Ala Ala Val Ser Tyr Ser His Gln Ser Thr Ala Thr Leu Thr
 1250 1255 1260
 Pro Ser Pro Gln Glu Glu Leu Gln Pro Met Leu Gln Asp Cys Pro Glu
 1265 1270 1275 1280
 Glu Thr Gly His Met Gln His Gln Pro Asp Arg Arg Arg Gln Pro Val
 1285 1290 1295
 Ser Pro Pro Pro Pro Pro Arg Pro Ile Ser Pro Pro His Thr Tyr Gly
 1300 1305 1310
 Tyr Ile Ser Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu
 1315 1320 1325
 Glu Glu Glu Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg
 1330 1335 1340
 Arg Leu Leu Leu Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly
 1345 1350 1355 1360
 Asp Leu Glu Ser Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser
 1365 1370 1375
 Ala Ser Glu Glu Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser
 1380 1385 1390
 Ser Asp Gly Ser Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala
 1395 1400 1405
 Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln
 1410 1415 1420
 Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro
 1425 1430 1435 1440
 Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln
 1445 1450 1455
 Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg
 1460 1465 1470
 Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro
 1475 1480 1485
 Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg
 1490 1495 1500

Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Arg
 1505 1510 1515 1520
 Ser Ser Asp Arg Lys Gly Ser Ser Tyr Lys Gly Arg Glu Val Leu Asp
 1525 1530 1535
 Gly Arg Gln Val Val Asp Met Arg Thr Asn Pro Gly Asp Pro Arg Glu
 1540 1545 1550
 Ala Gln Glu Gln Gln Asn Asp Gly Lys Gly Arg Gly Asn Lys Ala Ala
 1555 1560 1565
 Lys Arg Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile
 1570 1575 1580
 Leu Pro Tyr Cys Arg Pro Thr Phe Pro Thr Ser Asn Asn Pro Arg Asp
 1585 1590 1595 1600
 Pro Ser Ser Ser Ser Ser Met Ser Ser Arg Gly Ser Gly Ser Arg Gln
 1605 1610 1615
 Arg Glu Gln Ala Asn Val Gly Arg Arg Asn Ile Ala Glu Met Gln Val
 1620 1625 1630
 Leu Gly Gly Tyr Glu Arg Gly Glu Asp Asn Asn Glu Glu Leu Glu Glu
 1635 1640 1645
 Thr Glu Ser
 1650

<210> 9
 <211> 854
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> human roundabout (robo) 2 partial cDNA

<400> 9
 cagattgttg ctcaagggtcg aacagtgaca tttccctgtg aaactaaagg aaaccacag 60
 ccagctgttt tttggcagaa agaaggcagc cagaacctac ttttcccaa ccaaccccag 120
 cagcccaaca gtagatgtc agtgtcacca actggagacc tcacaatcac caacattcaa 180
 cgttccgacg cgggttacta catctgccag gctttaaact tggcaggaag catttttagca 240
 aaagctcaac tggaggttac tgatgttttg acagatagac ctccacctat aattctacaa 300
 ggcccagcca accaaacgct ggcagtggat ggtacagcgt tactgaaatg taaagccact 360
 ggtgatcctc ttctgtaat tagctgggta aaggagggat ttacttttcc gggtagagat 420
 ccaagagcaa caattcaaga gcaaggcaca ctgcagatta agaatttacg gatttctgat 480
 actggcactt atacttgtgt ggctacaagt tcaagtggag aggcttcctg gagtgcagtg 540
 ctggatgtga cagagtctgg agcaacaatc agtaaaaact atgatttaag tgacctgcca 600
 gggccaccat ccaaaccgca agtcactgat gttactaaga acagtgtcac cttgtcctgg 660
 cagccaggta cccttgaac ccttcagca agtgcatata tcattgaggc tttcagccaa 720
 tcagttagca acagctggca gaccgtggca aaccatgtaa agaccaccct ctatactgta 780
 agaggactgc ggccaatac aatctactta ttcatgtgtca gagcgatcaa cccaaggtg 840
 tcagtgaccc aagt 854

<210> 10
 <211> 284
 <212> PRT
 <213> Homo sapiens

<220>

<223> human roundabout (robo) 2 (H2) protein

<400> 10

Gln	Ile	Val	Ala	Gln	Gly	Arg	Thr	Val	Thr	Phe	Pro	Cys	Glu	Thr	Lys	
1				5					10					15		
Gly	Asn	Pro	Gln	Pro	Ala	Val	Phe	Trp	Gln	Lys	Glu	Gly	Ser	Gln	Asn	
			20					25					30			
Leu	Leu	Phe	Pro	Asn	Gln	Pro	Gln	Gln	Pro	Asn	Ser	Arg	Cys	Ser	Val	
		35					40					45				
Ser	Pro	Thr	Gly	Asp	Leu	Thr	Ile	Thr	Asn	Ile	Gln	Arg	Ser	Asp	Ala	
	50					55					60					
Gly	Tyr	Tyr	Ile	Cys	Gln	Ala	Leu	Thr	Val	Ala	Gly	Ser	Ile	Leu	Ala	
65					70					75					80	
Lys	Ala	Gln	Leu	Glu	Val	Thr	Asp	Val	Leu	Thr	Asp	Arg	Pro	Pro	Pro	
				85					90					95		
Ile	Ile	Leu	Gln	Gly	Pro	Ala	Asn	Gln	Thr	Leu	Ala	Val	Asp	Gly	Thr	
			100					105					110			
Ala	Leu	Cys	Lys	Cys	Lys	Ala	Thr	Gly	Asp	Pro	Leu	Pro	Val	Ile	Ser	
		115						120				125				
Trp	Leu	Lys	Glu	Gly	Phe	Thr	Phe	Pro	Gly	Arg	Asp	Pro	Arg	Ala	Thr	
	130					135					140					
Ile	Gln	Glu	Gln	Gly	Thr	Leu	Gln	Ile	Lys	Asn	Leu	Arg	Ile	Ser	Asp	
145					150					155					160	
Thr	Gly	Thr	Tyr	Thr	Cys	Val	Ala	Thr	Ser	Ser	Ser	Gly	Glu	Ala	Ser	
				165					170					175		
Trp	Ser	Ala	Val	Leu	Asp	Val	Thr	Glu	Ser	Gly	Ala	Thr	Ile	Ser	Lys	
			180					185					190			
Asn	Tyr	Asp	Leu	Ser	Asp	Leu	Pro	Gly	Pro	Pro	Ser	Lys	Pro	Gln	Val	
		195					200					205				
Thr	Asp	Val	Thr	Lys	Asn	Ser	Val	Thr	Leu	Ser	Trp	Gln	Pro	Gly	Thr	
	210					215					220					
Pro	Gly	Thr	Leu	Pro	Ala	Ser	Ala	Tyr	Ile	Ile	Glu	Ala	Phe	Ser	Gln	
225					230					235					240	
Ser	Val	Ser	Asn	Ser	Trp	Gln	Thr	Val	Ala	Asn	His	Val	Lys	Thr	Thr	
				245					250					255		
Leu	Tyr	Thr	Val	Arg	Gly	Leu	Arg	Pro	Asn	Thr	Ile	Tyr	Leu	Phe	Met	
			260					265					270			
Val	Arg	Ala	Ile	Asn	Pro	Lys	Val	Ser	Val	Thr	Gln					
		275					280									

<210> 11
 <211> 444
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse roundabout (robo) 1 cDNA

<400> 11
 gccaggcag ttgctgcagc tgcggagtat gcgggcctga aagtggctcg ccgccaaatg 60
 caagatgctg ctggccgccc ccacttccat gcctctcagt gcccaaggcc cagcagtcct 120
 gtgtccacag acagcaacat gagtgtgtgt gtgatccaga aagccagacc cgccaagaag 180
 cagaaacacc agccaggaca tctgcgcagg gaagcctacg cagatgatct tccaccccct 240
 ccagtgccac cacctgctat aaaatcgccc actgtccagt ccaaggcaca gctggaggta 300
 cggcctgtca tgggtccaaa actcgcgtct atagaagcaa ggacagatag atcgtcagac 360
 agaaaaggag gcagttacaa ggggagagaa gctctggatg gaagacaagt cactgacctg 420
 cgaacaaatc caagtgaccc caga 444

<210> 12
 <211> 148
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse roundabout (robo) 1 protein

<400> 12
 Ala Gln Ala Val Ala Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala
 1 5 10 15
 Arg Arg Gln Met Gln Asp Ala Ala Gly Arg Arg His Phe His Ala Ser
 20 25 30
 Gln Cys Pro Arg Pro Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser
 35 40 45
 Ala Val Val Ile Gln Lys Ala Arg Pro Ala Lys Lys Gln Lys His Gln
 50 55 60
 Pro Gly His Leu Arg Arg Glu Ala Tyr Ala Asp Asp Leu Pro Pro Pro
 65 70 75 80
 Pro Val Pro Pro Pro Ala Ile Lys Ser Pro Thr Val Gln Ser Lys Ala
 85 90 95
 Gln Leu Glu Val Arg Pro Val Met Val Pro Lys Leu Ala Ser Ile Glu
 100 105 110
 Ala Arg Thr Asp Arg Ser Ser Asp Arg Lys Gly Gly Ser Tyr Lys Gly
 115 120 125
 Arg Glu Ala Leu Asp Gly Arg Gln Val Thr Asp Leu Arg Thr Asn Pro
 130 135 140
 Ser Asp Pro Arg
 145

<210> 13
 <211> 909
 <212> PRT
 <213> Caenorhabditis elegans

<220>
 <223> C. elegans roundabout (robo) (CE) protein

<400> 13
 Met Phe Asn Arg Lys Thr Leu Leu Cys Thr Ile Leu Leu Val Leu Gln
 1 5 10 15
 Ala Val Ile Arg Ser Phe Cys Glu Asp Ala Ser Asn Leu Ala Pro Val
 20 25 30
 Ile Ile Glu His Pro Ile Asp Val Val Val Ser Arg Gly Ser Pro Ala
 35 40 45
 Thr Leu Asn Cys Gly Ala Lys Pro Ser Thr Ala Lys Ile Thr Trp Tyr
 50 55 60
 Lys Asp Gly Gln Pro Val Ile Thr Asn Lys Glu Gln Val Asn Ser His
 65 70 75 80
 Arg Ile Val Leu Asp Thr Gly Ser Leu Phe Leu Leu Lys Val Asn Ser
 85 90 95
 Gly Lys Asn Gly Lys Asp Ser Asp Ala Gly Ala Tyr Tyr Cys Val Ala
 100 105 110
 Ser Asn Glu His Gly Glu Val Lys Ser Asn Glu Gly Ser Leu Lys Leu
 115 120 125
 Ala Met Leu Arg Glu Asp Phe Arg Val Arg Pro Arg Thr Val Gln Ala
 130 135 140
 Leu Gly Gly Glu Met Ala Val Leu Glu Cys Ser Pro Pro Arg Gly Phe
 145 150 155 160
 Pro Glu Pro Val Val Ser Trp Arg Lys Asp Asp Lys Glu Leu Arg Ile
 165 170 175
 Gln Asp Met Pro Arg Tyr Thr Leu His Ser Asp Gly Asn Leu Ile Ile
 180 185 190
 Asp Pro Val Asp Arg Ser Asp Ser Gly Thr Tyr Gln Cys Val Ala Asn
 195 200 205
 Asn Met Val Gly Glu Arg Val Ser Asn Pro Ala Arg Leu Ser Val Phe
 210 215 220
 Glu Lys Pro Lys Phe Glu Gln Glu Pro Lys Asp Met Thr Val Asp Val
 225 230 235 240
 Gly Ala Ala Val Leu Phe Asp Cys Arg Val Thr Gly Asp Pro Gln Pro
 245 250 255
 Gln Ile Thr Trp Lys Arg Lys Asn Glu Pro Met Pro Val Thr Arg Ala
 260 265 270

Tyr Ile Ala Lys Asp Asn Arg Gly Leu Arg Ile Glu Arg Val Gln Pro
 275 280 285
 Ser Asp Glu Gly Glu Tyr Val Cys Tyr Ala Arg Asn Pro Ala Gly Thr
 290 295 300
 Leu Glu Ala Ser Ala His Leu Arg Val Gln Ala Pro Pro Ser Phe Gln
 305 310 315 320
 Thr Lys Pro Ala Asp Gln Ser Val Pro Ala Gly Gly Thr Ala Thr Phe
 325 330 335
 Glu Cys Thr Leu Val Gly Gln Pro Ser Pro Ala Tyr Phe Trp Ser Lys
 340 345 350
 Glu Gly Gln Gln Asp Leu Leu Phe Pro Ser Tyr Val Ser Ala Asp Gly
 355 360 365
 Arg Thr Lys Val Ser Pro Thr Gly Thr Leu Thr Ile Glu Glu Val Arg
 370 375 380
 Gln Val Asp Glu Gly Ala Tyr Val Cys Ala Gly Met Asn Ser Ala Gly
 385 390 395 400
 Ser Ser Leu Ser Lys Ala Ala Leu Lys Val Thr Thr Lys Ala Val Thr
 405 410 415
 Gly Asn Thr Pro Ala Lys Pro Pro Pro Thr Ile Glu His Gly His Gln
 420 425 430
 Asn Gln Thr Leu Met Val Gly Ser Ser Ala Ile Leu Pro Cys Gln Ala
 435 440 445
 Ser Gly Lys Pro Thr Pro Gly Ile Ser Trp Leu Arg Asp Gly Leu Pro
 450 455 460
 Ile Asp Ile Thr Asp Ser Arg Ile Ser Gln His Ser Thr Gly Ser Leu
 465 470 475 480
 His Ile Ala Asp Leu Lys Lys Pro Asp Thr Gly Val Tyr Thr Cys Ile
 485 490 495
 Ala Lys Asn Glu Asp Gly Glu Ser Thr Trp Ser Ala Ser Leu Thr Val
 500 505 510
 Glu Asp His Thr Ser Asn Ala Gln Phe Val Arg Met Pro Asp Pro Ser
 515 520 525
 Asn Phe Pro Ser Ser Pro Thr Gln Pro Ile Ile Val Asn Val Thr Asp
 530 535 540
 Thr Glu Val Glu Leu His Trp Asn Ala Pro Ser Thr Ser Gly Ala Gly
 545 550 555 560
 Pro Ile Thr Gly Tyr Ile Ile Gln Tyr Tyr Ser Pro Asp Leu Gly Gln
 565 570 575
 Thr Trp Phe Asn Ile Pro Asp Tyr Val Ala Ser Thr Glu Tyr Arg Ile
 580 585 590

Lys Gly Leu Lys Pro Ser His Ser Tyr Met Phe Val Ile Arg Ala Glu
 595 600 605
 Asn Glu Lys Gly Ile Gly Thr Pro Ser Val Ser Ser Ala Leu Val Thr
 610 615 620
 Thr Ser Lys Pro Ala Ala Gln Val Ala Leu Ser Asp Lys Asn Lys Met
 625 630 635 640
 Asp Met Ala Ile Ala Glu Lys Arg Leu Thr Ser Glu Gln Leu Ile Lys
 645 650 655
 Leu Glu Glu Val Lys Thr Ile Asn Ser Thr Ala Val Arg Leu Phe Trp
 660 665 670
 Lys Lys Arg Lys Leu Glu Glu Leu Ile Asp Gly Tyr Tyr Ile Lys Trp
 675 680 685
 Arg Gly Pro Pro Arg Thr Asn Asp Asn Gln Tyr Val Asn Val Thr Ser
 690 695 700
 Pro Ser Thr Glu Asn Tyr Val Val Ser Asn Leu Met Pro Phe Thr Asn
 705 710 715 720
 Tyr Glu Phe Phe Val Ile Pro Tyr His Ser Gly Val His Ser Ile His
 725 730 735
 Gly Ala Pro Ser Asn Ser Met Asp Val Leu Thr Ala Glu Ala Pro Pro
 740 745 750
 Ser Leu Pro Pro Glu Asp Val Arg Ile Arg Met Leu Asn Leu Thr Thr
 755 760 765
 Leu Arg Ile Ser Trp Lys Ala Pro Lys Ala Asp Gly Ile Asn Gly Ile
 770 775 780
 Leu Lys Gly Phe Gln Ile Val Ile Val Gly Gln Ala Pro Asn Asn Asn
 785 790 795 800
 Arg Asn Ile Thr Thr Asn Glu Arg Ala Ala Ser Val Thr Leu Phe His
 805 810 815
 Leu Val Thr Gly Met Thr Tyr Lys Ile Arg Val Ala Ala Arg Ser Asn
 820 825 830
 Gly Gly Val Gly Val Ser His Gly Thr Ser Glu Val Ile Met Asn Gln
 835 840 845
 Asp Thr Leu Glu Lys His Leu Ala Ala Gln Gln Glu Asn Glu Ser Phe
 850 855 860
 Leu Tyr Gly Leu Ile Asn Lys Ser His Val Pro Val Ile Val Ile Val
 865 870 875 880
 Ala Ile Leu Ile Ile Phe Val Val Ile Ile Ile Ala Tyr Cys Tyr Trp
 885 890 895
 Arg Asn Ser Arg Asn Ser Asp Gly Lys Asp Arg Ser Phe
 900 905

<210> 14
 <211> 883
 <212> PRT
 <213> *Drosophila melanogaster*

 <220>
 <223> *Drosophila* roundabout (robo) 2 (D2) protein

 <400> 14
 Gly Glu Asn Pro Arg Ile Ile Glu His Pro Met Asp Thr Thr Val Pro
 1 5 10 15
 Lys Asn Asp Pro Phe Thr Phe Asn Cys Gln Ala Glu Gly Asn Pro Thr
 20 25 30
 Pro Thr Ile Gln Trp Phe Lys Asp Gly Arg Glu Leu Lys Thr Asp Thr
 35 40 45
 Gly Ser His Arg Ile Met Leu Pro Ala Gly Gly Leu Phe Phe Leu Lys
 50 55 60
 Val Ile His Ser Arg Arg Glu Ser Asp Ala Gly Thr Tyr Trp Cys Glu
 65 70 75 80
 Ala Lys Asn Glu Phe Gly Val Ala Arg Ser Arg Asn Ala Thr Leu Gln
 85 90 95
 Val Ala Val Leu Arg Asp Glu Phe Arg Leu Glu Pro Ala Asn Thr Arg
 100 105 110
 Val Ala Gln Gly Glu Val Ala Leu Met Glu Cys Gly Ala Pro Arg Gly
 115 120 125
 Ser Pro Glu Pro Gln Ile Ser Trp Arg Lys Asn Gly Gln Thr Leu Asn
 130 135 140
 Leu Val Gly Asn Lys Arg Ile Arg Ile Val Asp Gly Gly Asn Leu Ala
 145 150 155 160
 Ile Gln Glu Ala Arg Gln Ser Asp Asp Gly Arg Tyr Gln Cys Val Val
 165 170 175
 Lys Asn Val Val Gly Thr Arg Glu Ser Ala Thr Ala Phe Leu Lys Val
 180 185 190
 His Val Arg Pro Phe Leu Ile Arg Gly Pro Gln Asn Gln Thr Ala Val
 195 200 205
 Val Gly Ser Ser Val Val Phe Gln Cys Arg Ile Gly Gly Asp Pro Leu
 210 215 220
 Pro Asp Val Leu Trp Arg Arg Thr Ala Ser Gly Gly Asn Met Pro Leu
 225 230 235 240
 Arg Lys Phe Ser Trp Leu His Ser Ala Ser Gly Arg Val His Val Leu
 245 250 255
 Glu Asp Arg Ser Leu Lys Leu Asp Asp Val Thr Leu Glu Asp Met Gly
 260 265 270

Glu Tyr Thr Cys Glu Ala Asp Asn Ala Val Gly Gly Ile Thr Ala Thr
 275 280 285
 Gly Ile Leu Thr Val His Ala Pro Pro Lys Phe Val Ile Arg Pro Lys
 290 295 300
 Asn Gln Leu Val Glu Ile Gly Asp Glu Val Leu Phe Glu Cys Gln Ala
 305 310 315 320
 Asn Gly His Pro Arg Pro Thr Leu Tyr Trp Ser Val Glu Gly Asn Ser
 325 330 335
 Ser Leu Leu Leu Pro Gly Tyr Arg Asp Gly Arg Met Glu Val Thr Leu
 340 345 350
 Thr Pro Glu Gly Arg Ser Val Leu Ser Ile Ala Arg Phe Ala Arg Glu
 355 360 365
 Asp Ser Gly Lys Val Val Thr Cys Asn Ala Leu Asn Ala Val Gly Ser
 370 375 380
 Val Ser Ser Arg Thr Val Val Ser Val Asp Thr Gln Phe Glu Leu Pro
 385 390 395 400
 Pro Pro Ile Ile Glu Gln Gly Pro Val Asn Gln Thr Leu Pro Val Lys
 405 410 415
 Ser Ile Val Val Leu Pro Cys Arg Thr Leu Gly Thr Pro Val Pro Gln
 420 425 430
 Val Ser Trp Tyr Leu Asp Gly Ile Pro Ile Asp Val Gln Glu His Glu
 435 440 445
 Arg Arg Asn Leu Ser Asp Ala Gly Ala Leu Thr Ile Ser Asp Leu Gln
 450 455 460
 Arg His Glu Asp Glu Gly Leu Tyr Thr Cys Val Ala Ser Asn Arg Asn
 465 470 475 480
 Gly Lys Ser Ser Trp Ser Gly Tyr Leu Arg Leu Asp Thr Pro Thr Asn
 485 490 495
 Pro Asn Ile Lys Phe Phe Arg Ala Pro Glu Leu Ser Thr Tyr Pro Gly
 500 505 510
 Pro Pro Gly Lys Pro Gln Met Val Glu Lys Gly Glu Asn Ser Val Thr
 515 520 525
 Leu Ser Trp Thr Arg Ser Asn Lys Val Gly Gly Ser Ser Leu Val Gly
 530 535 540
 Tyr Val Ile Glu Met Phe Gly Lys Asn Glu Thr Asp Gly Trp Val Ala
 545 550 555 560
 Val Gly Thr Arg Val Gln Asn Thr Thr Phe Thr Gln Thr Gly Leu Leu
 565 570 575
 Pro Gly Val Asn Tyr Phe Phe Leu Ile Arg Ala Glu Asn Ser His Gly
 580 585 590

Leu Ser Leu Pro Ser Pro Met Ser Glu Pro Ile Thr Val Gly Thr Arg
 595 600 605
 Tyr Phe Asn Ser Gly Leu Asp Leu Ser Glu Ala Arg Ala Ser Leu Leu
 610 615 620
 Ser Gly Asp Val Val Glu Leu Ser Asn Ala Ser Val Val Asp Ser Thr
 625 630 635 640
 Ser Met Lys Leu Thr Trp Gln Ile Ile Asn Gly Lys Tyr Val Glu Gly
 645 650 655
 Phe Tyr Val Tyr Ala Arg Gln Leu Pro Asn Pro Leu Asn Thr Lys Tyr
 660 665 670
 Arg Met Leu Thr Ile Leu Asn Gly Gly Gly Ala Ser Ser Cys Thr Ile
 675 680 685
 Thr Gly Leu Val Gln Tyr Thr Leu Tyr Glu Phe Phe Ile Val Pro Phe
 690 695 700
 Tyr Lys Ser Val Glu Gly Lys Pro Ser Asn Ser Arg Ile Ala Arg Thr
 705 710 715 720
 Leu Glu Asp Val Pro Ser Glu Ala Pro Tyr Gly Met Glu Ala Leu Leu
 725 730 735
 Leu Asn Ser Ser Ala Val Phe Leu Lys Trp Lys Ala Pro Glu Leu Lys
 740 745 750
 Asp Arg His Gly Val Leu Leu Asn Tyr His Val Ile Val Arg Gly Ile
 755 760 765
 Asp Thr Ala His Asn Phe Ser Arg Ile Leu Thr Asn Val Thr Ile Asp
 770 775 780
 Ala Ala Ser Pro Thr Leu Val Leu Ala Asn Leu Thr Glu Gly Val Met
 785 790 795 800
 Tyr Thr Val Gly Val Ala Ala Gly Asn Asn Ala Gly Val Gly Pro Tyr
 805 810 815
 Cys Val Pro Ala Thr Leu Arg Leu Asp Pro Ile Thr Lys Arg Leu Asp
 820 825 830
 Pro Phe Ile Asn Gln Arg Asp His Val Asn Asp Val Leu Thr Gln Pro
 835 840 845
 Trp Phe Ile Ile Ile Leu Gly Ala Ile Leu Ala Val Leu Met Leu Ser
 850 855 860
 Phe Gly Ala Met Val Phe Val Lys Arg Lys His Met Met Met Lys Gln
 865 870 875 880
 Ser Ala Leu

<210> 15
 <211> 330
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human roundabout (robo) 2 partial cDNA

<400> 15
 aaaccacaga aaaacaatgg atccacttgg gccaatgtcc ctctacctcc cccccagtc 60
 cagccccttc ctggcacgga gctggaacac tatgcagtgg aacaacaaga aaatggctat 120
 gacagtgata gctgggtgcc accattgcca gtacaaactt acttacacca aggtctggaa 180
 gatgaactgg aagaagatga tgataggggtc ccaacacctc ctgttcgagg cgtggcttct 240
 tctcctgcta tctcctttgg acagcagtcc actgcaactc ttactccatc cccacgggaa 300
 gagatgcaac ccatgctgca ggcttcacct 330

<210> 16
 <211> 114
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human roundabout (robo) 2 partial cDNA

<400> 16
 ttacctcct ctcaaagacc tcgacctacc agcccatttt ctactgacag taacaccagt 60
 gcagccctga gtcaaagtca gaggcctcgg ccactaaaa aacacaaggg aggg 114

<210> 17
 <211> 110
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human roundabout (robo) 2 partial protein

<400> 17
 Lys Pro Gln Lys Asn Asn Gly Ser Thr Trp Ala Asn Val Pro Leu Pro
 1 5 10 15
 Pro Pro Pro Val Gln Pro Leu Pro Gly Thr Glu Leu Glu His Tyr Ala
 20 25 30
 Val Glu Gln Gln Glu Asn Gly Tyr Asp Ser Asp Ser Trp Cys Pro Pro
 35 40 45
 Leu Pro Val Gln Thr Tyr Leu His Gln Gly Leu Glu Asp Glu Leu Glu
 50 55 60
 Glu Asp Asp Asp Arg Val Pro Thr Pro Pro Val Arg Gly Val Ala Ser
 65 70 75 80
 Ser Pro Ala Ile Ser Phe Gly Gln Gln Ser Thr Ala Thr Leu Thr Pro
 85 90 95
 Ser Pro Arg Glu Glu Met Gln Pro Met Leu Gln Ala Ser Pro
 100 105 110

<210> 18
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human roundabout (robo) 2 partial protein

<400> 18
 Phe Thr Ser Ser Gln Arg Pro Arg Pro Thr Ser Pro Phe Ser Thr Asp
 1 5 10 15
 Ser Asn Thr Ser Ala Ala Leu Ser Gln Ser Gln Arg Pro Arg Pro Thr
 20 25 30
 Lys Lys His Lys Gly Gly
 35

<210> 19
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <223> H-Robo1 (502-651)

<400> 19
 Leu Arg Asp Asp Phe Arg Gln Asn Pro Ser Asp Val Met Val Ala Val
 1 5 10 15
 Gly Glu Pro Ala Val Met Glu Cys Gln Pro Pro Arg Gly His Pro Glu
 20 25 30
 Pro Thr Ile Ser Trp Lys Lys Asp Gly Ser Pro Leu Asp Asp Lys Asp
 35 40 45
 Glu Arg
 50

<210> 20
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <223> EST:yu23d11 H77734

<400> 20
 Leu Arg Asp Asp Phe Arg Gln Lys Pro Ser Asp Val Met Val Ala Val
 1 5 10 15
 Gly Glu Pro Ala Val Met Glu Cys Gln Pro Pro Arg Gly His Pro Glu
 20 25 30
 Pro Thr Ile Ser Trp Lys Lys Asp Gly Ser Pro Leu Asp Asp Lys Asp
 35 40 45
 Glu Arg
 50

<210> 21
 <211> 50
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> H-Robol (502-651)

 <400> 21
 tacttcggga tgacttcaga caaaaacctt cggatgtcat ggttgcagta 50

 <210> 22
 <211> 50
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> EST:yu23d11 H77734

 <400> 22
 tacttcggga tgacttcaga caaaaacctt cggatgtcat ggttgcagta 50

 <210> 23
 <211> 16
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> EST:yu23d11 H7734

 <400> 23
 Leu Arg Asp Asp Phe Arg Gln Lys Pro Ser Asp Val Met Val Ala Val
 1 5 10 15

 <210> 24
 <211> 205
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> H-Robol

 <400> 24
 Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu Glu Glu Glu
 1 5 10 15
 Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg Arg Leu Leu
 20 25 30
 Leu Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly Asp Leu Glu
 35 40 45
 Ser Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser Ala Ser Glu
 50 55 60
 Glu Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser Ser Asp Gly
 65 70 75 80

Ser Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala Ala Ala Ala
 85 90 95
 Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln Asp Ala Ala
 100 105 110
 Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro Thr Ser Pro
 115 120 125
 Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln Lys Thr Arg
 130 135 140
 Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg Arg Glu Thr
 145 150 155 160
 Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro Ala Ile Lys
 165 170 175
 Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg Pro Val Val
 180 185 190
 Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Lys
 195 200 205

<210> 25
 <211> 134
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> EST:yq76e12 H52936

<400> 25
 Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu Glu Glu Glu
 1 5 10 15
 Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg Leu Leu Leu
 20 25 30
 Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly Asp Leu Glu Ser
 35 40 45
 Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser Ala Ser Glu Glu
 50 55 60
 Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser Ser Asp Gly Ser
 65 70 75 80
 Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala Ala Ala Ala Glu
 85 90 95
 Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln Asp Ala Ala Gly
 100 105 110
 Arg Arg His Phe His Ala Phe Gln Cys Pro Arg Pro Thr Ser Pro Val
 115 120 125
 Phe Thr Asp Ser Asn Met
 130

<210> 26
 <211> 114
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> EST:yq76e12 H52937

 <220>
 <221> MOD_RES
 <222> (1)..(6)
 <223> Xaa = unknown amino acid

 <400> 26
 Xaa Ala Ala Thr Ala Xaa Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln
 1 5 10 15
 Met Arg Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro
 20 25 30
 Arg Pro Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val
 35 40 45
 Met Gln Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His
 50 55 60
 Leu Arg Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro
 65 70 75 80
 Pro Pro Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu
 85 90 95
 Val Arg Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr
 100 105 110
 Asp Lys

<210> 27
 <211> 303
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hybridization
 probe for human roundabout 1 immunoglobulin domain
 #1

<400> 27
 ccacctcgca ttgttgaaca cccttcagac ctgattgtct caaaaggaga acctgcaact 60
 ttgaactgca aagctgaagg ccgcccaca cccactattg aatggtacaa agggggagag 120
 agagtggaga cagacaaaga tgaccctcgc tcacaccgaa tgttgctgcc gactggatct 180
 ttatttttct tacgtatagt acatggacgg aaaagtagac ctgatgaagg agtctatgtc 240
 tgtgtagcaa ggaattacct tggagaggct gtgagccaca atgcatcgct ggaagtagcc 300
 ata 303

<210> 28
 <211> 275
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybridization
probe for human roundabout 1 immunoglobulin domain
#2

<400> 28

```
cttcgggatg acttcagaca aaacccttcg gatgtcatgg ttgcagtagg agagcctgca 60
gtaatggaat gccaacctcc acgaggccat cctgagccca ccatttcatg gaagaaagat 120
ggctctccac tggatgataa agatgaaaga ataactatac gaggaggaaa gctcatgatc 180
acttacaccc gtaaaagtga cgctggcaaa tatgtttgtg ttggtaccaa tatggttggg 240
gaacgtgaga gtgaagtagc cgagctgact gtctt 275
```

<210> 29

<211> 273

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybridization
probe for human roundabout 1 immunoglobulin domain
#3

<400> 29

```
agagagacca tcatttgtga agagaccag taacttggca gtaactgtgg atgacagtgc 60
agaatttaaa tgtgaggccc gaggtgacct tgtacctaca gtacgatgga ggaaagatga 120
tggagagctg cccaaatcca gatatgaaat ccgagatgat cataccttga aaattaggaa 180
ggtgacagct ggtgacatgg gtccatacac ttgtgttgca gaaaatatgg tgggcaaagc 240
tgaagcatct gctactctga ctgttcaaga acc 273
```

<210> 30

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybridization
probe for human roundabout 1 immunoglobulin domain
#4

<400> 30

```
ccacattttg ttgtgaaacc ccgtgaccag gttgttgctt tgggacggac tgtaactttt 60
cagtgtgaag caaccggaag tcctcaacca gctattttct ggaggagaga agggagtcag 120
aatctacttt tctcatatca accaccacag tcatccagcc gattttcagt ctcccagact 180
ggcgacctca caattactaa tgtccagcga tctgatgttg gttattacat ctgccagact 240
ttaaattgtt ctggaagcat catcacaag gcatatttgg aagttacaga tgtgattgca 300
```

<210> 31

<211> 286

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybridization
probe for human roundabout 1 immunoglobulin domain
#5

<400> 31

```
gatcggcctc cccagttat tcgacaaggt cctgtgaatc agactgtagc cgtggatggc 60
```

```

acttttcgtcc tcagctgtgt ggccacaggc agtccagtgc ccaccattct gtggagaaaag 120
gatggagtcc tcgtttcaac ccaagactct cgaatcaaac agttggagaa tggagtactg 180
cagatccgat atgctaagct ggggtgatact ggtcgggtaca cctgcattgc atcaaccccc 240
agtgggtgaag caacatggag tgcttacatt gaagttcaag aatttg 286

```

```

<210> 32
<211> 297
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:hybridization
      probe for human roundabout 1 fibronectin domain #1

```

```

<400> 32
gagttccagt tcagcctcca agacctactg acccaaattt aatccctagt gccccatcaa 60
aacctgaagt gacagatgtc agcagaaata cagtcacatt atcgtggcaa ccaaatttga 120
attcaggagc aactccaaca tcttatatta tagaagcctt cagccatgca tctggtagca 180
gctggcagac cgtagcagag aatgtgaaaa cagaaacatc tgccattaaa ggactcaaac 240
ctaattgcaat ttaccttttc cttgtgaggg cagctaattg atatggaatt agtgatc 297

```

```

<210> 33
<211> 351
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:hybridization
      probe for human roundabout 1 fibronectin domain #2

```

```

<400> 33
caagccaaat atcagatcca gtgaaaacac aagatgtcct accaacaagt caggggggtg 60
accacaagca ggtccagaga gagctgggaa atgctgttct gcacctccac aacccccaccg 120
tcctttcttc ctcttccatc gaagtgcact ggacagtaga tcaacagtct cagtatatac 180
aaggatataa aattctctat cggccatctg gagccaacca cggagaatca gactgggttag 240
tttttgaaat gaggacgcca gccaaaaaca gtgtggtaat ccctgatctc agaaagggag 300
tcaactatga aattaaggct cgcccttttt ttaatgaatt tcaaggagca g 351

```

```

<210> 34
<211> 305
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:hybridization
      probe for human roundabout 1 fibronectin domain #3

```

```

<400> 34
atagtgaat caagtttgcc aaaaccctgg aagaagcacc cagtgcccca cccaaggtg 60
taactgtatc caagaatgat ggaaacggaa ctgcaattct agttagttag cagccacctc 120
cagaagacac tcaaaatgga atggtccaag agtataaggt ttggtgtctg ggcaatgaaa 180
ctcgatacca catcaacaaa acagtggatg gttccacctt ttccgtgggc attccctttc 240
ttgttcctgg aatccgatac agtgtggaag tggcagccag cactggggct ggggtctgggg 300
taaag 305

```


<210> 35
 <211> 100
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:hybridization
 probe for human roundabout 1 transmembrane domain

 <400> 35
 agatttcaga tgtggtgaag cagccggcct tcatagcagg tattggagca gcctggtgga 60
 tcacctcat ggtcttcagc atctggcttt atcgacaccg 100

 <210> 36
 <211> 100
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:hybridization
 probe for human roundabout 1 cytoplasmic motif #1

 <400> 36
 aatctgaagg atgggcgttt tgtcaatcca tcagggcagc ctactcctta cgccaccact 60
 cagctcatcc agtcaaact cagcaacaac atgaacaatg 100

 <210> 37
 <211> 100
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:hybridization
 probe for human roundabout 1 cytoplasmic motif #2

 <400> 37
 cccaaggtac caaaacaggg tggcatgaac tgggcagacc tgcttcctcc tccccagca 60
 catcctctc cacacagcaa tagcgaagag tacaacattt 100

 <210> 38
 <211> 100
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:hybridization
 probe for human roundabout 1 cytoplasmic motif #3

 <400> 38
 ccagccagga catctgcgca gagaaacct cagagatgat cttccaccac ctctgtgcc 60
 gccacctgct ataaagtcac ctactgccca atccaagaca 100

 <210> 39
 <211> 273
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybridization
probe for human roundabout 2 immunoglobulin domain
#4

<400> 39

```
cagattgttg ctcaaggctg aacagtgaca tttccctgtg aaactaaagg aaacccacag 60
ccagctgttt tttggcagaa agaaggcagc cagaacctac ttttcccaa ccaaccccag 120
cagcccaaca gtagatgctc agtgtcacca actggagacc tcacaatcac caacattcaa 180
cgttccgacg cgggttacta catctgccag gctttaactg tggcaggaag catttttagca 240
aaagctcaac tggaggttac tgatgttttg aca                                     273
```

<210> 40

<211> 285

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybridization
probe for human roundabout 2 immunoglobulin domain
#5

<400> 40

```
gatagacctc cacctataat tctacaaggc ccagccaacc aaacgctggc agtggatggt 60
acagcgttac tgaaatgtaa agccactggt gatcctcttc ctgtaattag ctgggttaaag 120
gagggattta cttttccggg tagagatcca agagcaacaa ttcaagagca aggcacactg 180
cagattaaga atttacggat ttctgatact ggcacttata cttgtgtggc tacaagttca 240
agtggagagg cttcctggag tgcagtgtcg gatgtgacag agtct                                     285
```

<210> 41

<211> 296

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybridization
probe for human roundabout 2 fibronectin domain #1

<400> 41

```
ggagcaacaa tcagtaaaaa ctatgattta agtgacctgc cagggccacc atccaaaccg 60
caagtcactg atgttactaa gaacagtgtc accttgtcct ggcagccagg tacccttgga 120
acccttccag caagtgcata tatcattgag gctttcagcc aatcagtgag caacagctgg 180
cagaccgtgg caaacatgtt aaagaccacc ctctatactg taagaggact gcggcccaat 240
acaatctact tattcatggt cagagcgatc aacccaagg tytcagtgac ccaagt       296
```

<210> 42

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:human
roundabout 1 immunoglobulin domain #1 PCR forward
primer

<400> 42

ccacctcgca ttgttgaaca cccttcagac

30

<210> 43
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout 1 immunoglobulin domain #1 PCR reverse
 primer

 <400> 43
 atggctactt ccagcgatgc attgtggctc 30

 <210> 44
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout 1 immunoglobulin domain #2 PCR forward
 primer

 <400> 44
 cttcgggatg acttcagaca aaacccttcg 30

 <210> 45
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout 1 immunoglobulin domain #2 PCR reverse
 primer

 <400> 45
 taagacagtc agctcggcta cttcactctc 30

 <210> 46
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout 1 immunoglobulin domain #3 PCR forward
 primer

 <400> 46
 agagagacca tcatttgtga agagaccag 30

 <210> 47
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 immunoglobulin domain #3 PCR reverse
 primer

<400> 47
 aggttcttga acagtcagag tagcagatgc 30

<210> 48
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 immunoglobulin domain #4 PCR forward
 primer

<400> 48
 ccacattttg ttgtgaaacc ccgtgaccag 30

<210> 49
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 immunoglobulin domain #4 PCR reverse
 primer

<400> 49
 tgcaatcaca tctgtaactt ccaaatatgc 30

<210> 50
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 immunoglobulin domain #5 PCR forward
 primer

<400> 50
 atcggcctcc ccagttatt cgacaaggtc 30

<210> 51
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 immunoglobulin domain #5 PCR reverse
 primer

<400> 51
 caaattcttg aacttcaatg taagcactcc 30

<210> 52
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 fibronectin domain #1 PCR forward
 primer

<400> 52
 gagttccagt tcagcctcca agacctactg 30

<210> 53
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 fibronectin domain #1 PCR reverse
 primer

<400> 53
 tcactaattc catatgcatt agctgccctc 30

<210> 54
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 fibronectin domain #2 PCR forward
 primer

<400> 54
 caagccaaat atcagatcca gtgaaaacac 30

<210> 55
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 fibronectin domain #2 PCR reverse
 primer

<400> 55
 atctgctcct tgaaattcat taaaaaaagg 30

<210> 56
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout 1 fibronectin domain #3 PCR forward
 primer

 <400> 56
 atagtgaat caagtttgcc aaaaccctg 29

 <210> 57
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout 1 fibronectin domain #3 PCR reverse
 primer

 <400> 57
 ctctttaccc cagaccagc ccagtgctg 30

 <210> 58
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout 1 transmembrane domain PCR forward
 primer

 <400> 58
 ggaccaagtc agcctcgctc agcagatttc 30

 <210> 59
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout 1 transmembrane domain PCR reverse
 primer

 <400> 59
 actagtaagt ccgtttctct tcttgcggtg 30

 <210> 60
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 cytoplasmic motif #1 PCR forward
 primer

<400> 60
 ctgaaggatg ggcgttttgt caatccatc 29

<210> 61
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 cytoplasmic motif #1 PCR reverse
 primer

<400> 61
 gtcccagtgg tttccagtgc ttctcgccag 30

<210> 62
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 cytoplasmic motif #2 PCR forward
 primer

<400> 62
 ggacaagaa aggggcaaga acaccaagg 30

<210> 63
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 cytoplasmic motif #2 PCR reverse
 primer

<400> 63
 atagctttca tctacagaaa tgttgtactc 30

<210> 64
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 cytoplasmic motif #3 PCR forward
 primer

<400> 64
 accagaccag ccaagaaact gaaacaccag 30

<210> 65
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 1 cytoplasmic motif #3 PCR reverse
 primer

<400> 65
 gtacttccag ctgtgtcttg gattgggcag 30

<210> 66
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 2 immunoglobulin domain #4 PCR forward
 primer

<400> 66
 gttgctcaag gtcgaacagt gacatttccc 30

<210> 67
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 2 immunoglobulin domain #4 PCR reverse
 primer

<400> 67
 tgtcaaaaca tcagtaacct ccagttgagc 30

<210> 68
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:human
 roundabout 2 immunoglobulin domain #5 PCR forward
 primer

<400> 68
 gatagacctc cacctataat tctacaaggc 30

<210> 69
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout 2 immunoglobulin domain #5 PCR reverse
 primer

 <400> 69
 gactctgtca catccagcac tgcactccag 30

 <210> 70
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout 2 fibronectin domain #1 PCR forward
 primer

 <400> 70
 caatcagtaa aaactatgat ttaagtg 27

 <210> 71
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout 2 fibronectin domain #1 PCR reverse
 primer

 <400> 71
 tcgctctgac catgaataag tagattg 27

 <210> 72
 <211> 17
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Drosophila
 roundabout-I conserved cytoplasmic motif #1

 <400> 72
 Pro Asp Asn Pro Thr Pro Tyr Ala Thr Thr Met Ile Ile Gly Thr Ser
 1 5 10 15
 Ser

<210> 73
 <211> 17
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 roundabout-I conserved cytoplasmic motif #1

 <400> 73
 Ser Gly Gln Pro Thr Pro Tyr Ala Thr Thr Gln Leu Ile Gln Ser Asn
 1 5 10 15

 Leu

 <210> 74
 <211> 17
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Drosophila
 roundabout-II conserved cytoplasmic motif #1

 <400> 74
 Asn Ala Ser Pro Ala Pro Tyr Ala Thr Ser Ser Ile Leu Ser Pro His
 1 5 10 15

 Gln

 <210> 75
 <211> 17
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C. elegans
 roundabout conserved cytoplasmic motif #1

 <400> 75
 His Asp Asp Pro Ser Pro Tyr Ala Thr Thr Thr Leu Val Leu Ser Asn
 1 5 10 15

 Gln

 <210> 76
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:consensus
 roundabout conserved cytoplasmic motif #1

 <220>
 <221> MOD_RES
 <222> (8)
 <223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (9)..(10)
<223> Xaa = Ile, Leu or Val

<400> 76
Pro Thr Pro Tyr Ala Thr Thr Xaa Xaa Xaa
1 5 10

<210> 77
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Drosophila
roundabout-I conserved cytoplasmic motif #2

<400> 77
Ile Asn Trp Ser Glu Phe Leu Pro Pro Pro Glu His Pro Pro Pro
1 5 10 15

Ser Ser Thr Tyr Gly Tyr
20

<210> 78
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
roundabout-I conserved cytoplasmic motif #2

<400> 78
Met Asn Trp Ala Asp Leu Leu Pro Pro Pro Pro Ala His Pro Pro Pro
1 5 10 15

His Ser Asn Ser Glu Glu Tyr
20

<210> 79
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
roundabout-II conserved cytoplasmic motif #2

<400> 79
Ser Thr Trp Ala Asn Val Pro Leu Pro Pro Pro Pro Val Gln Pro Leu
1 5 10 15

Pro Gly Thr Glu Leu Glu His Tyr
20

<210> 80
<211> 22
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:C. elegans
roundabout conserved cytoplasmic motif #2

<400> 80

Lys Thr Leu Met Asp Phe Ile Pro Pro Pro Pro Ser Asn Pro Pro Pro
1 5 10 15

Pro Gly Gly His Val Tyr
20

<210> 81
<211> 23
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
roundabout conserved cytoplasmic motif #2

<220>

<221> MOD_RES

<222> (3)..(5)

<223> Xaa = any amino acid

<220>

<221> MOD_RES

<222> (6)..(7)

<223> Xaa = hydrophobic amino acid

<220>

<221> MOD_RES

<222> (12)..(22)

<223> Xaa = any amino acid

<400> 81

Asn Trp Xaa Xaa Xaa Xaa Xaa Pro Pro Pro Pro Xaa Xaa Pro Pro Pro
1 5 10 15

Xaa Ser Xaa Xaa Xaa Xaa Tyr
20

<210> 82
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Drosophila
roundabout-I conserved cytoplasmic motif #3

<400> 82
Pro Ser Pro Met Gln Pro Pro Pro Pro Val Pro Val Pro Glu Gly Trp
1 5 10 15

Tyr

<210> 83
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
roundabout-I conserved cytoplasmic motif #3

<400> 83
Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro Ala Ile Lys
1 5 10 15

Ser Pro

<210> 84
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mouse
roundabout-I conserved cytoplasmic motif #3

<400> 84
Tyr Ala Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro Ala Ile Lys
1 5 10 15

Ser Pro

<210> 85
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:C. elegans
roundabout conserved cytoplasmic motif #3

<400> 85
Arg Ala Pro Ala Met Pro Thr Asn Pro Val Pro Pro Glu Pro Pro Ala
1 5 10 15

Arg Tyr

<210> 86
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 roundabout conserved cytoplasmic motif #3

 <400> 86
 Pro Pro Pro Pro Val Pro Pro Pro
 1 5

 <210> 87
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:conserved
 cytoplasmic motif #2 binding site for Drosophila
 Enabled protein

 <400> 87
 Leu Pro Pro Pro
 1

 <210> 88
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:ROBO6 PCR
 primer specific for region flanking CfoI
 polymorphism

 <400> 88
 gcattggggtc atctgtagag 20

 <210> 89
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:ROBO23 PCR
 primer specific for region flanking CfoI
 polymorphism

 <400> 89
 agctatctgg agggagggcat 20

 <210> 90
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:D-robo ORF PCR
 amplification primer

<400> 90
gagtgggtgaa ttcaacagca ccaaaaccac aaaatgcatc cc 42

<210> 91
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:D-robo ORF PCR
amplification primer

<400> 91
cggggagtct agaacacttc atccttaggt g 31

<210> 92
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:six histidine
fusion protein tag

<400> 92
His His His His His His
1 5